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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
           Copyright
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OM protein - protein search, using sw model Run

November 17, 2005, 06:38:35 . ::

; Search time 90.8333 Seconds (without alignments)
464.112 Million cell updates/sec

US-09-674-857-1 Perfect score:

1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKAK 109 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

2105692 segs, 386760381 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:* geneseqp2003bs:* Genesed 16Dec04:* geneseqp1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Ads84436 Human ant	. m	Aam47857 Human Ig-	Abg30462 Human ant	Abg77148 Anti-IGF-	Aae32916 Human imm	Aae32628 Human imm	4 Human	Ade97353 Human IgG	2 Human	1541 Anti-i	Adq95469 Human IgG	3562 Human	Aay06895 Human IL-	Aar26782 CD4-gamma	Aar46678 CD4-gamma	Aay85079 Human CD4	Aab67322 CD4-gamma	Aab80883 Human CD4
ADS84436	AAE02643	AAM47857	ABG30462	ABG77148	AAE32916	AAE32628	AAO30894	ADE97353	ADF75002	ADM41541	ADQ95469	ADR28562	AAY06895	AAR26782	AAR46678	AAY85079	AAB67322	AAB80883
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26	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	

ALIGNMENTS

AAY54996 standard; protein; 109 AA. RESULT 1 AAY54996

(first entry) 17-FEB-2000

Mutated CH2 sequence Gideltaab.

Binding molecule, CH2 sequence, complement dependent lysis, FegammaRIIb, cell-mediated destruction, human; immunoglobulin G; IgG heavy chain, B cell activation, mast cell degranulation; phagocytosis, vasculitis, Crohn's disease; graft-vs-host disease; organ transplant rejection, bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; sucoimmune thrombocytopaenia, arthritis; erythroblastosis foetalis; sickle cell anaemia; coronary artery occlusion.

Synthetic.

WO9958572-A1.

18-NOV-1999.

99WO-GB001441. 07-MAY-1999; 98GB-00009951. 08-MAY-1998; (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

Williamson LM; Clark MR, Armour KL,

WPI; 2000-039075/03.

Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties.

Claim 12; Fig 17; 81pp; English.

This sequence represents the mutated CH2 molecule Gideltaab, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant

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domain of a human immunoglobulin G (1gG) heavy chain. The binding molecule is used to bind a target molecule (especially FegammaRIIb causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding molecule e.g. an antibody, to the target molecule. The binding molecule e.g. an antibody, to the target molecule. The binding molecule is useful for the treatment of graft-vs-nost disease, organ transplant rejection, bone-marrow transplant rejection, autoimmune haromotytopaenia and arthritis) alloimmune haromotytopaenia and arthritis, alloimmunity (e.g. troinic or acute inflammatory diseases (e.g. Crohn's, HDN chroblasticosis focetalls), Goodpastures, sickle cell anaemia and coronary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FegammaR and desirable ing properties have been retained. The polypeptides do not contain nonlumnan amino acide, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent through interaction with FCRn contains.
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Sequence 109 AA;

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100.0%; Score 581; DB 3; Length 109; 100.0%; Pred. No. 7.5e-52;
                                      Indels
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                                      0; Mismatches
                Best Local Similarity 100.
Matches 109; Conservative
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Query Match
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AAE37576 standard; protein; 449 AA. 27-AUG-2003 AAE37576; AAE3757 RESULT

Human FD1D2-Ig alphatp fusion protein variant. (first entry)

Human, CD4; cluster of differentiation factor 4; immunoglobulin; Ig; human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; D1; D2; alpha tailpiece; alphatp; fusion protein; mutein; variant; mutant.

Homo sapiens

'note= "Wild type Leu substituted with Val" 'note= "Wild type Glu substituted with Pro' /note= "Wild type Gly substituted with Ala" Location/Qualifiers 218 Misc-difference 219 Key Misc-difference Misc-difference THE STATE OF THE S

WO2003040311-A2

15-MAY-2003.

25-OCT-2001; 2001US-0346231P. 24-OCT-2002; 2002WO-US034393

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Cicala C, Arthos J,

WPI; 2003-441545/41. N-PSDB; ACC82877.

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polypeptide ligated at the C-terminus with a portion of an immunoglobulin [19] comprising a hinge region and a constant domain of a mammalian Ig heavy chain. The polypeptide comprises a tailpiece from the C-terminus of the heavy chain of an IgA or IgM antibody. Polypeptides of the invention is useful for preparing a composition for treating or preventing human are useful for preparing a composition for treating or preventing human therapy and also in the preparation of vaccines. The present sequence is a fusion protein variant (G218P/L219V/220delA/G221A) which comprises a fusion protein is also referred to as mutant region. This variant protein is also referred to as mutant F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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                                                                                                                                                                                                                                 The invention relates to a CD4 (cluster of differentiation factor 4)
                               New CD4 polypeptide ligated at its C-terminus with a portion of an immunoglobulin, useful for preparing a composition for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenotransplantation; graft rejection; cell interaction; pig; vascular cell adhesion molecule; VCAM; monoclonal antibody; chimeric antibody; diagnosis.
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                                                                 immunoglobulin, useful for preventing HIV-1 infection.
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(first entry)
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Matches 106; Conservative
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                           A chimeric antibody (AAW14933) comprises the C1 and hinge regions of human 1gG2 and the C2 and C3 regions of human 1gG4 (G2/G4 MAb) and a murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal antibody (WAAD) 2A2 heavy chain variable region sequence also AAW14932). The chimeric antibody is specific for porcine VCAM. It is useful for diagnosing human rejection of porcine exentransplants and for improving xenotransplants on of porcine cells, tissues and for human recipients. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                  (see
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                                                                                                                                                                                                                                            Xenotransplantation; graft rejection; cell interaction; pig; vascular cell adhesion molecule; VCAM; monoclonal antibody; chimeric antibody; diagnosis.
                                                                                                                                                Length 462;
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                                                                                                                                                                    1; Indels
                                                                                                                                              Score 565; DB 2;
Pred. No. 1.9e-49;
2; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                 (Chimeric) human G2/G4 chimeric antibody.
        Disclosure; Page 42-44; 105pp; English.
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Best Local Similarity
Matches 106; Conserv
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26-SEP-1996;
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Chimeric.
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useful for diagnosing human rejection of porcine xenotransplants and for improving xenotransplantation of porcine cells, tissues and organs into human recipients. (Updated on 17-OCT-2003 to standardise OS field)
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vascular cell adhesion molecule; VCAM; monoclonal antibody;
chimeric antibody; diagnosis.
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                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                           Query Match
97.2%; Score 565; DB 2;
Best Local Similarity 97.2%; Pred. No. 1.9e-49;
Matches 106; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 565; DB 2;
Pred. No. 1.9e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3F4 (Chimeric) human G2/G4 chimeric antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 56-57; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW14939 standard; protein; 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US015575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
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308 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 356

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RESULT 7
ABP51695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A chimeric antibody (AAW14940) comprises the C1 and hinge regions of human 1gG2 and the C2 and C3 regions of human 1gG4 (G2/G4 MAb) and a murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal antibody (MAb) 3F4 heavy chain variable region sequence (see also AAW14938). The chimeric antibody is specific for porcine VCAM. It is useful for diagnosing human rejection of porcine exentransplants and for improving xenotransplants and for confinence (Updated on 17-OCT-2003 to standardise OS field)
                                                    248 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 307
                          APPVAGESVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibodies binding to porcine but not human cell interaction proteins useful to treat and assay for rejection of xenografted porcine organs, tissues or cells.
 Gaps
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 ö
                                                                                              REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rother RP,
                                                                                                                                                                                                                                                                                                       Xenotransplantation, graft rejection, cell interaction, pig,
vascular cell adhesion molecule, VCAM, monoclonal antibody,
chimeric antibody, diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.2%; Score 565; DB 2; Length 463; 97.2%; Pred. No. 1.9e-49;
                                                                                REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK
 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rollins S,
                                                                                                                                                                                                                                                                             3F4 (Chimeric) human G2/G4 chimeric antibody.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 58-61; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mueller EE,
                                                                                                                                                                                 Ź
2;
                                                                                                                                                                              AAW14940 standard; protein; 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US015575.
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                                                                                                                                                                                                                                                    (first entry)
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Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mueller JP, Evans MJ,
                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-212855/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT62937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 463 AA;
                                                                                                                                                                                                                                                                                                                                                                 Homo; sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      WO9711971-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-1996;
                                                                                                                                                                                                                                     17-OCT-2003
                                                                                                                                                                                                                                                   16-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-1997.
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Chimeric.
                                                                                                                                                                                                          AAW14940;
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The present into present the complementary determining region (DR) are present of the complementary determining region (CDR) are least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide complementary determining region (CDR) are minetic such as an erythropoletin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of the amentopoletic cells, and a stimulator of haematopolesis. (I) is useful for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with complements or megakaryocytes, where (I) is contacted with production. (I) with a region where amino acid residues corresponding to production of CDRs fused to an EPO mimetic, or which has one or component of its CDRs fused to an EPO mimetic, is useful for increasing the production of red blood cells, where (I) is contacted with haematopoietic content of the progenitors. (I) is useful for increasing the content of the progenitors (I) is useful for diagnostics or therapeutics, in cell isolation strategies, and for treating patients or appression of haematopoietic contents related to the suppression of haematopoiesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an immunoglobin molecule or its fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or
                                                                                                                                                                     TPO; BPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
                                                                                                                            5G1.1-TPO heavy chain amino acid sequence SEQ ID NO:67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Renshaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barbas-Frederickson S,
ABP51695 standard; protein; 472 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Fig 13A; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-DEC-2000; 2000US-0251448P.
04-MAY-2001; 2001US-028889P.
29-MAY-2001; 2001US-0294068P.
                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-2001; 2001WO-US047656
                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombopoetin mimetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-566610/60.
N-PSDB; ABQ73374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 472 AA;
                                                                                                                                                                                                                                                                                                                             WO200246238-A2.
                                                                                                                                                                                                                                                                sapiens.
                                                                                    01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š,
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                                                                                                                                                                                                                                                                                       Synthetic
                                        ABP51695;
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Gaps

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5; Length 472; 1; Indels

Score 565; DB 5; Pred. No. 2e-49; 2; Mismatches

97.2%; 97.2%;

Query Match
Best Local Similarity 97.23
Matches 106; Conservative

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Gaps

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1; Indels

2; Mismatches

Conservative

Local Similarity Les 106; Conserv

9

REEQYNSIYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109

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1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP

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                                                                                                                                                                                                                                                                                 WO2003093319-A1.
                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                            26-FEB-2004
                                                                                                                                                                                                                                                                                                              13-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                        Jalkanen S,
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                                                             ADF77155;
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ADQ17121
   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDR8) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents an immunoglobulin antibody heavy chain of
immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive; immunotherapy; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with BPO mimetic or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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                                                                            REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin antibody 5G1.1-TPO heavy chain SEQ ID NO:67.
                                                               REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8; Length 472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 565; DB o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2e-4
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Renshaw M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO 67; 107pp; English
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                                                                                                                                                                     ADQ16647 standard; protein; 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.2%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-2003; 2003WO-US036894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-2002; 2002US-00307724
                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.2
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-460973/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADQ16648.
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                                                                                                                                                                                                                                                                                                                                                                                          WO2004050017-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bowdish KS,
                                                                                                                                                                                                                                    09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                     ADQ16647;
                                                                                          317
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                                                                                                                                                         ADQ1664
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This sequence represents the constant region of a human anti-Vascular Adhesion Protein-1 (VAP-1) antibody heavy chain. This sequence may be used in the production of a chimeric mouse-human anti-VAP-1 antibody. The nucleic acid molecules, polypeptides or antibodies are useful in treating VAP-1 mediated inflammatory disorders, such as rheumatoid arthritis, inflammatory bowel disease, autoimmune diseases or psoriasis. The chimeric VAP-1 antibody is further used for in viro and in vivo diagnostic applications, including in vivo immunoscintigraphic imaging of inflammation sites. The chimeric MAD's of the invention have improved kinetic properties compared to the corresponding murine antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and encoding nucleic acid molecules, useful for diagnosing and treating chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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                                                                                                                                                                                                                                                complementarity determining region; CDR; mouse; Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain; chimeric; inflammatory disorder; rheumatoid arthritis; inflammatory bowel disease; autoimmune disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised anti-NGF antibody E3 heavy chain full-length protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                        Anti-VAP-1 monoclonal antibody H chain constant
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ADF77155 standard; protein; 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-APR-2002; 2002FI-00000807.
                                                                                                                                                                                                                                                                                                                                                                                    immunoscintigraphic imaging.
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Matches 104; Conservative
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                                                                                                                             entry)
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Shelton DL, Pons J, Rosenthal A;
                                                                                                                                                              (RINA-) RINAT NEUROSCIENCE CORP.
                 mouse; mutant; mutein
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                                                                                                                                                                           WPI; 2004-525786/50.
N-PSDB; ADQ17170.
                                                                                                     Misc-difference 101
                                                  Misc-difference
                                                                                Misc-difference
                                                                                                                Misc-difference
                                                                       Misc-difference
                                                                                                                             WO2004058184-A2
                          Homo sapiens.
Synthetic.
                                                                                                                                   15-JUL-2004.
                                                                                                                                                                                             pain, or f
arthritis.
                        gb.
                                         Region
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/note= "Extended CDR (complementarity determining region)
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/note= "Extended CDR (complementarity determining region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild-type Ile of murine Mab 911 substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Wild-type Met of murine Mab 911 substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild-type Leu of murine Mab 911 substituted by
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nerve growth factor; anti-NGF antibody; El3.5 trigeminal neurone; analgesic; immunomedulator; post-surgical pain; rheumatoid arthritis; osteoarthritis; inflammatory cachexia; gene therapy; monoclonal antibody 911; humanised antibody E3; heavy chain; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Wild-type Tyr of murine Mab 911 substituted
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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28-JAN-2003; 2003US-0443522P. 08-OCT-2003; 2003US-0510006P. 24-DEC-2002; 2002US-0436905P. 24-DEC-2003; 2003WO-US041252

New anti-nerve growth factor antibodies for preventing or treating pain, including post-surgical pain, rheumatoid arthritis pain or osteoarthritis pain, or for treating inflammatory cachexia associated with rheumatoid

Claim 25; SEQ ID NO 16; 186pp; English.

The invention relates to a novel anti-nerve growth factor (NGF) antibody which binds NGF with a KD of less than about 2 nM and inhibits human NGF-dependent survival of mouse E13.5 trigeminal neurones with an ICSO of about 100 or 10 pM or less, where the ICSO is measured in the presence of about 15 or 1.5 pM of human NGF. The antibody of the invention demonstrates analgesic and immunomodulator activities and may be useful for preventing and/or treating pain, including post-surgical pain and pain associated with rheumatoid arthritis or osteoarthritis. The antibody may be further utilised for treating inflammatory cachexia associated with rheumatoid arthritis, as well as during gene therapy procedures. The current sequence is that of the humanised antibody E3 heavy chain full-length protein of the invention which was synthesised via

Sequence 462 AA

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                                                                                                                                                                                                                   232 APPVAGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPBVQFNWYVDGVEVHNAKTKP 291
                                                                                                                                                                                  9
       from murine anti-NGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and encoding nucleic acid molecules, useful for diagnosing and treating chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.
                                                                                                                                                                                1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complementarity determining region; CDR; mouse;
Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;
chimeric; inflammatory disorder; rheumatoid arthritis;
inflammatory bownel disease; autoimmune disease; psoriasis;
immunoscintigraphic imaging.
   grafting CDRs (complementarity determining regions) from murine and (monoclonal antibody) 911 onto human framework seguences and subsequently mutating the CDRs to improve binding.
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                                                                                                                                                                                                                                                                       292 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 340
                                                                                                                                                                                                                                                      61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                             Length 447;
                                                                                                         Score 562; DB 8; Length 44
Pred. No. 3.8e-49;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric Anti-VAP-1 monoclonal antibody H chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; SEQ ID NO 15; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laukkanen M,
                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                             ADF77154 standard; peptide; 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-2002; 2002FI-00000807.
                                                                                                       Query Match 96.7%;
Best Local Similarity 95.4%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-022642/02.
N-PSDB; ADF77144.
                                                                                                       Query Match
Best Local Similarity
                                                                      Sequence 447 AA;
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grafting (
Mab (monoo
                                                                                                                                                                                                                                                                                                                                                                                                                ADF77154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric.
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the mutated CH2 molecule Gldeltaac, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant domain of a human immunoglobulin (G (IgG) heavy chain. The binding molecule is used to bind a target molecule (especially FcgammaRID molecule is used to bind a target molecule (especially FcgammaRID molecule is used to binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit can of a second binding molecule can be used to prevent or inhibit the binding molecule is useful for the treatment of graft-vs-coluctule. The binding molecule is useful for the treatment of graft-vs-coluction, autoimmune transplant rejection, bone-marrow transplant rejection, autoimmune hamolytic anaemia, contoinmune thrombocytopaenia, and arthritis), alloimmune thrombocytopaenia, act asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN cerythroblastosis foetalis), Goodpastures, sickle cell anaemia and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Binding molecule; CH2 sequence; complement dependent lysis; FogammaRIIb; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis, vasculitis; Crohn's disease; graft-va-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopaemia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopaemia; goodpastures disease; therapy;
                                                                                                                                          Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties.
                                                                                                       1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                           Gaps
                                                           ö
                                                                                                                                                                                                                                            307 REEQFNSTFRVVSVLTVVHQDMLNGKEYKCKVSNKGLPSSIEKTISKTK 355
                                                                                                                                                                                                              61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
        Length 462;
                                                           1; Indels
  96.7%; Score 562; DB 8;
95.4%; Pred. No. 4e-49;
ive 4; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sickle cell anaemia; coronary artery occlusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark MR, Williamson LM;
                                                                                                                                                                                                                                                                                                                                                                                               AAY54998 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Fig 17; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutated CH2 sequence Gldeltaac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-GB001441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                         Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-039075/03
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Armour KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY54998;
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coronary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through PcgammaR and desirable IgG properties have been retained. The polypeptides do not contain non-uman amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent with being able to cross the human placenta through interaction with FCRn (neonatal FC receptor)
                                                                                                                                                                                                                                                                                                                                                                   59
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                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVAGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                   1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erythropoietin; EPO; immunoglobulin; IgG;
fragment crystallisation region; FC; chronic anaemia; renal disease;
cancer chemotherapy; rheumatoid arthritis; AIDS;
myelodysplastic syndrome; (HuEPO)-L-vFcgamma2; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                 DB 3; Length 110;
                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                         96.3%; Score 559.5; DB 3 98.2%; Pred. No. 1.2e-49; Live 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human HuEPO-L-vFcgamma2 fusion protein.
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/note= "EPO"
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                                                                                                                                                                                                                                                               Query Match 96.3
Best Local Similarity 98.2
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note=
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SUN B N C.
SUN C R Y.
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                                                                                                                                                                                                                 Sequence 110 AA;
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The invention relates to a recombinant human erythropoietin (HuEPO) -L-vFC fusion protein comprising HuEPO, a peptide linker, and a human CC fusion protein Comprising HuEPO, a peptide linker, and a human cC immunoglobulin GFC (fragment crystallisation reggion) variant. Also included is a carbohydrate-derived cell line producing the human ccreates of 10 microgramme per million cells in a 24-hour period. The HuEPO c excess of 10 microgramme per million cells in a 24-hour period. The HuEPO c excess of 10 microgramme per million cells in a 24-hour period. The HuEPO c of at least 2-fold relative to that of recombinant HuEPO on a molar comprise the period linker containing about 20 or fewer amino cacids is present between HuEPO and the human IGG FC variant. The IGG FC contains amino acid mutations to attenuate effector functions. The human IGG with comprises a hinge, CH2 and CH3 domains of human IGG with CFC variant comprises a hinge, CH2 and CH3 domains of human IGG with CFC variant comprises a hinge, CH2 and CH3 domains of human IGG with CFC contains amino acid mutations, human IGG with Ser228Pro and Leu235Ala mutations, or human IGG1 with Leu234Val, Leu235Ala and Pro331Ser mutations. The CFC cecombinant human erythropoietin-L-vFC fusion protein in treating patients with chronic anaemia caused by renal failure, cancer crecombinant human erythropoietin-L-vFC fusion protein in the serum, as compared to prior art, leads to lower dosages and less frequent injections result in better patient compliance and quality, of life. The concentrations means improved safety and tolerability, and less frequent injections result in better patient compliance and quality of life. The present sequence represents the fusion protein HUEPO-L-vFCgamma2. Claim 3; Fig 2A; 14pp; English

Seguence 436 AA;

221 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 280 9 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP ö REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109 281 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPASIEKTISKTK 329 96.2%; Score 559; DB 7; Length 436; 94.5%; Pred. No. 7.5e-49; live 5; Mismatches 1; Indels = Conservative Local Similarity nes 103; Conserv 61 Query Match Matches g ò 용

ADR48984 standard; protein; 436 AA ADR48984;

HuEPO-L-Fc fusion protein.

(first entry)

02-DEC-2004

antianaemic, nephrotropic, human, HuBPO-L-vFc, erythropoietin, BPO, anaemia, renal disease, cancer chemotherapy, rheumatoid arthritis, AZT treatment, HIV infection, myelodysplastic syndrome, renal failure.

Homo sapiens

Synthetic.

US2004175824-A1.

09-SEP-2004.

21-JAN-2004; 2004US-00761593

17-AUG-2001; 2001US-00932812

SUN L K. SUN B N C. SUN C R Y. (SUNL/) (SUNC/)

Sun CRY; Sun BNC, Sun LK,

WPI; 2004-634851/61. N-PSDB; ADR48983 New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin (HuEPO), a peptide linker, and a human IgG Fc variant, useful for treating chronic anemia due to renal diseases, cancer chemotherapy, or rheumatoid arthritis.

Claim 3; SEQ ID NO 18; 31pp; English.

A recombinant HuBPO-L-vFc fusion protein comprises human erythropoietin (HuBPO).

Charles a peptide linker, and a human 1gG Fc variant, is new.

INDEPROBRY CLAMAS are also included for the following: a chinese hammer over yet (CO)-derived cell line producing the HuBPO-L-vFc fusion protein in the peptide linker, and a human 1gG Fc variant. Preferred protein: The peptide linker, and a human 1gG Fc variant. Preferred protein: The peptide linker containing 20 or fewer amino acids is present mino acids selected from glycine, estine, alanine, and threonine. The muman 1gG Fc variant, and Comprises two or more amino acids selected from glycine, estine, alanine, and threonine. The muman 1gG Fc variant comprises a hinge, CH3, and CH3 domains of human 1gG with Pro313Ear mutations comprising 437 amino acids (SBQ ID NO. 18).

CC comprises a hinge, CH2, and CH3 domains of human 1gG with leads activity similar too higger than the of fruge on a molar cological activity similar too higger than that of fruge on a molar cological activity similar too higger than that of fruge on a molar cological activity similar too higger than that of fruge on a molar cological activity similar too higger than that of fruge on a molar cological activity similar too higger than that of fruge on a molar cological activity similar too higger than that of fruge on a molar cological activity similar too higger than the of fruge on a molar contribute of the log Fc contains amino acid mutations to attended min nexcess of 30 kmicrosy ger million cells in a 24 hour period. The human 1gG Fc contains amino acid mutations to attended the functions, a flexible peptide linker companies a hinge, CH3.

CC To the log Fc contains amino acid mutations to attended the functions, a flexible peptide linker companies. The function and the human 1gG Fc variant comprises a hinge, CH3.

CC To the log Fc variant comprises a molar basis. Antiamented the free growth medium in excess of 10 kmicrosy general generating a cuttor of mutation or mycle of the cortain exhibits in For the convenience of cloning, SEQ ID NO. 1 which incorporates a restriction enzyme cleavage site is used as the 5' oligonucleotide primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon and incorporates a BamHI site. The resulting DNA fragments of approximately 600 bp were inserted into a holding vector such as pUC19 at the HindIII and BamHI sites to give the DBPO plasmid. The sequence of the human EPO gene was confirmed by DNA sequencing.

Sequence 436 AA;

. 0 Length 436; Indels Query Match 96.2%; Score 559; DB 8; Lv Best Local Similarity 94.5%; Pred. No. 7.5e-49; Matches 103; Conservative 5; Mismatches 1;

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233 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 292
                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPASIEKTISKTK 341
                                                                                                                                            Length 448;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                ï
                                                                                                                                       Score 559; DB 7;
Pred. No. 7.8e-49;
5; Mismatches 1;
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                                                                                                                                       96.2%;
94.5%;
                                                                                                                                  Query Match
Best Local Similarity 94.5
Matches 103; Conservative
                                                       Sequence 448 AA;
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          X S
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stimulating factor (hG-CSF)-L-vFc fusion protein comprising hG-CSF, a
peptide linker, and a human immunoglobuling (IgG) Fc variant. Also
described are: a CHO-derived cell line producing the above hG-CSF-L-vFc
fusion protein in its growth medium in excess of 10 £mg/sg per million
cells in a 24-hour period; and making the recombinant fusion protein
cited above, comprising generating a CHO-derived cell line cited above,
growing the cell line under conditions the recombinant fusion protein is
expressed in its growth medium, and purifying the expressed protein. The
recombinant fusion protein is useful in treating a variety of conditions
associated with an impaired immune or haematopoietic system, including
cancer chemotherapy. leukaemias, anaemias, ALDS, bone marrow
transplantation, and chronic neutropenias. This is the amino acid
sequence of human GCSF-L-fragment of crystallisation gamma 2 variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-vFc fusion protein for treating immune or hemaropoietic system disorders comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin G Fc variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; immunostimulant; antianaemic; anti-HIV; protein therapy; human; granulocyte colony-stimulating factor; GCSF; GCSF-L-vFc; immunoglobulin G; IgG; fragment of cryetallisation; immune disorder; haematopoietic disorder; cancer; chemotherapy; leukaemia; anaemia; AIDS; bone marrow transplantation; chronic neutropenia; fusion protein; fragment of crystallisation gamma 2; Fc gamma 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mature human GCSF-L-fragment of crystallisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human GCSF-L-fragment of crystallisation gamma 2 fusion protein.
61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
281 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPASIEKTISKTK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Wild type Pro substituted by Ser"
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/label= GCSF leader peptide
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                                                                                                                                                                                                                                                                                                                                          ADM33376 standard; protein; 448 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma 2 fusion"
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/note= "M
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N-PSDB; ADM33375.
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(SUNB/) SUN B N C.
(SUNC/) SUN C R Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ADM33376;
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                                                                                                                                                                                                                                                RESULT 15
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                   Copyright
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OM protein - protein search, using sw model

November 17, 2005, 06:49:37; Search time 17.9178 Seconds (without alignments) 585.319 Million cell updates/sec Run on:

US-09-674-857-1 Title:

581 1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKAK 109 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% '
Maximum Match 100%
Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Ig gamma-2 chain C	-			Ig heavy chain V r	gamma-4 chain				gamma 2b	-	gamma 4	gamma 3	gamma	heavy	gamma-		ס	b	m	g gamma-	g heavy ch	מ	g gamma-1	gamma-1	noclonal a		Ig gamma-2a chain	ф
	, QI	G2HU	PT0207	S31866	GHHU	869339	G4HU	A23511	A60764	G3HUWI	147160	147159	147162	147161	147158	S22080	PS0018	GZGP	GHRB	S06611	G3MSC	G3MSM	C30554	S31459	GIMS	GIMSM	PC4436	S00847	G2MSAB	G2MSBM
	8	-+	7	4	-	~	٦	7	N	٦	~	~	7	~	N	7	~	٦	ч	N	٦	٦	~	~	Н	-	7	~	Н	-
	Match Length	326	234	255	330	374	327	377	377	289	328	328	277	328	328	470	333	329	323	327	329	398	308	472	N	393		329		
* 6	Match	95.4	93.8	93.5	93.5	93.5	92.9		90.5			78.8	78.0	76.1	76.1	٠.	72.3	71.8	71.1	70.7	70.7	70.7		•			68.2	67.5	65.7	65.7
	Score	554	545	543	543	543	540	524	524	504	458	458	453	442	442	429	420	417	413	411	410.5	410.5	410	410	396	396	396	392	382	382
11.00	No.	٦	7	m	4	'n	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	53	24	52	56	27	28	29

υ	Ig gamma-2a chain Ig gamma-2a chain	Ig gamma-2a chain Ig gamma-2b chain	Ig gamma-2a chain Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b, chain	Ig gamma heavy cha	ig epsilon-chain - Ig epsilon chain C	Ig gamma-1 chain C	Ig heavy chain pre	Ig epsilon chain C
G2MS11 PS0017	G2MSA G2MSAM	S37483 S01321	S40295 PS0019	B30503	A30503	146732	136948 EHHU	S14236	S04845	EHRT
4.0		77	~	1 (7	7	~	~ -	N	~	7
474 326	330 399	469	322	112	88	180	4 2 4 2 6 8 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	152	549	429
65.7	64.9 64.9	64.9 63.3	63.2	53.2	47.5	42.9	28.8	27.9	27.0	26.3
382 380	377	377	367	308	276	249	167.5	162	157	153
30	33 33	34 35	36	38	39	40	4 4 1 2	43	44	45

ALIGNMENTS

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GRHUU
C.Species Homos appleans (man)
C.Date: 30-Apr.1981 #Beagenenc revision 13-Jun-1983 #text_change 09-Jul-2004
C.Accession: A39306; A92809; A92809; A93132; A02148
P.E.Lison, J.: Hood, L.
Proc. Mall. Acad. & A. 79, 1984-1988, 1982
A.Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain cont A;Residence number: A9306; MUID:8197621; PMID:6504948
A.Accession: A9306
A.Motecule type: DAA
A.Gross-references: UNIPROT: PO1889; GB:V00554; GB:J00230; NID:932759; PIDN:CABS8438.1; P)
A.Accession: A9306
A.Motecule type: DAA
A.Gross-references: UNIPROT: PAROVE OF the human IGG2 heavy chain: genetic, evolutionary, and fit A: Members: A02809; MIID:81007873; PMID:6774012
A.Motecule type: protein
A.Accession: A9309
A.Title: The primary structure of a human IGG2 heavy chain constant region domains of a h.Accession: A9309
A.Title: The protein
A.Motecule type: protein
A.Mote
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A;Reference number: A94591 A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268 A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic

ned
R:Milatein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds

22 94

Gaps

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R'Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a caparence number: S33887, MUID:83001943; PMID:6811139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 88-113;235-330 < TAK>
A; Residues: 88-113;235-330 < TAK>
A; Residues: 88-113;235-330 < TAK>
A; Residues: BB1:217370
B; Cumningham, B.A.; Rittishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C.Biochemistry 9, 3161-3170, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequent A; Reference number: A90563; MUID:71064024; PMID:5489771
A; Rontents: myeloma protein Bu A; Recession: B90563
A; Rolecule type: protein
A; Rolecul
                        method for protein-protein interactions of cloned gene products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-310 < ELL.
A; Cross-references: UNIPROT: PO1857; EMBL: Z17370
A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers,
A; Note: Lys-330 is removed after translation
A; Note: Lys-330 is removed after translation
Submitted to the EMBL Data Library, October 1992
A; Reference number: S33904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Bate: 31-Jan-1981 #sequence revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93433; S3861; S3887; B90563; A90564; B91ē68; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PP-----VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                           A.Accession: 331866
A.Molecule type: mRNA
A.Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C.Keywords: immunoglobulin
F.1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A,Reference number: A93433; MUID:82274238; PMID:6287432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 93.5%; Score 543; DB 4; Length 255; Best Local Similarity 90.4%; Pred. No. 3e-46; Matches 103; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: S36861
A,Molecule type: DNA
Residuca: 2-30 cHAR>
A,Cross-references: EMBL:Z17370
                   A; Description: Screeing mel
A; Reference number: S31866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A93433
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                                                                                                                                                                                                                                                                                                          A,Coros-references: GDB:119338; OMIM:147110
A,Map position: 14q32.33-14q32.33
C,Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as 1gA and 1gM, the subunits associate into la C,Superfamily: immunoglobulin C region; immunoglobulin homology
C,Superfamily: immunoglobulin C region; immunoglobulin homology <IMI>
F,20-85/Domain: immunoglobulin homology <IMI>
F,33-306/Domain: immunoglobulin homology <IMI>
F,33-306/Domain: immunoglobulin homology <IMI>
F,34/Disulfide bonds: interchain (to light chain) #status experimental
F,27-83.140-200.246-304/Disulfide bonds: #status experimental
F,102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F,102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
PT0207
Ig gamma chain C region - chimpanzee
C; Species: Pan troglodytes (chimpanzee)
C; Species: Pan troglodytes (chimpanzee)
C; Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C; Accession: PT0207
R; Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A; Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A; Reference number: PT0207; MUID:91287716; PMID:2062315
A; Accession: PT0207
A; Molecule type: mRNA
A; Residues: 1-234 < EHR>
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 48-117/Domain: immunoglobulin homology <IMM>
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Ig gamma-1 chain C region - synthetic
C;Species: synthetic
C;Species: synthetic
C;Nocte: Note: New sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
R;Filpula, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 21, 145-148, 169
A;Ritel: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 93.6 Matches 102; Conservative
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요 8

ò 셤 A; Contents: Eu A; Accession: A90564

Best Local

g ò g ij

Gaps

9

22

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A,Map position: 14q12.33-14q32.33
A,Introns: 99/1, 111/1, 221/1
C,Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la c,Superfamily: immunoglobulin C region; immunoglobulin homology
C,Superfamily: immunoglobulin C region; heterotetramer; immunoglobulin P:20-85/Domain: immunoglobulin homology <IM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: the sequence was determined from the germline gene R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C. Botchen, J. 117, 33-47, 1970 Asidenen, J. 117, 33-47, 1970 Asidenen immunoglobulin sublclasses. Partial amino acid sequence of the constant A;Reference number: A90249; MUID:70207560; PMID:4192699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gramma-4 chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: John-1982 #sequence revision 02-Apr-1982 #sequence revision 02-Apr-1982 #sclison, J; Buxbaum, J; Hood, L. DNA 1, 11-18, 1981 A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene. A;Reference number: A90933; MUID:83157104; PMID:6299662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-317/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;107/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Redidues: 1-140, (2', 142-374 <KH2>
A;Csesidues: 1-140, (2', 142-374 <KH2>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 543; DB 2;
Pred. No. 4.7e-46;
2; Mismatches 3
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Pred. No. 7.9e-46;
                                                                                      Library, September 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861
                                                                                                                                                                                                                                                                                                                                                                                                                          93.5%;
90.4%;
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95.3%;
       A;Cross-references: EMBL:X81695 R;Khamlichi, A.A. submitted to the EMBL Data Libra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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A;Residues: 1-30;81-326 <PIN>
                                                                                                                      A; Reference number: S72664
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Best Local Similarity
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                                                                                                                                                                 A; Accession: S72664
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Best Local (
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                                                           dgen Primaeretruktur.

A, Reference number: A91668; MUID: 77070269; PMID: 826475

A, Reference number: A91668; MUID: 77070269; PMID: 826475

A, Rocession: B9166

A, Molecule type: protein

A, Molecule type: protein

A, Note: this sequence has the Glm(17) and Glm(1) markers

A, Note: this sequence has the Glm(17) and Glm(1) markers

B, Schmidt, W.E.; Jung, H.D.; Pallm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A, Title: Die Primaerstruktur des kristallisterbaren monoklonalen Immunglobulins IgG1 KOI

A, Reference number: A97723; MUID: 83289131; PMID: 6884994

A, Contents: myelona protein KOL; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-96, R', 99 197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A; Note: this sequence has the Glm(3) and Glm(non-1) markers
B; Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3186, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid A; Reference number: A90565; MUID:71064027, PMID:4923144
A; Contents: annotation; disulfide bonds
R; Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob enbromide cleavage products, and the disulfide bridges.
A; Reference number: A91667; MUID:77070267; PMID:1002129
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A/Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S65339
Ig heavy chain V region precursor - human
Is heavy chain V region precursor - human
C; Species: Homo saphens (man)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: S69339; S72664
B; Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A; Reference number: S69339; MUID:95262687; PMID:7744049
A; Reterence number: MNA
A; Residues: 1-374 < KHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PP----VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: IGHG1
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Best Local {
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Matches

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Gaps

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Ig gamma-3 heavy chain disease proteins - human
CiSpecias: Homo sapiens (man)
CiSpecias: Navol42; M92199; A93915; A02149
RiFrandione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304420, MUID: B1021548; PMID: 674477
A; Contents: heavy chain disease protein Wis
A; Contents: heavy chain disease protein Wis
A; Molecule type: protein
A; Rociesion: A9044
A; Molecule type: protein
A; Rociesion: A9044
A; Molecule type: protein
A; Rociesion: A9044
A; Molecule type: protein
A; Rociesion: Base a dimer linked by 12 disulfide bonds; it has an extra interchain
A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A; Note: the sequence of residues 42-76 was taken from the reference that follows
B; Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J; Biol. Chem. 252, 883-889, 197
A; Michaelsen, T.E.; Prangione, B.; Franklin, E.C.
A; Molecule type: protein
A; Reference number: A92219; MUID: 77118561; PMID: 402163
A; Molecule type: protein
A; Reference number: A92219; Muins, sequence corresponding to residues 12-97 of protein W; A; Molecule type: protein
A; Reference number: A92219
A; Molecule type: protein
A; Residues: 12-97 vallo
A; Molecule type: protein
A; Residues: 12-97 vallo
A; Molecule type: protein
A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A93915
A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157,,A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVQVHNAKTKPREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.7%; Score 504; DB 1;
86.8%; Pred. No. 2.5e-42;
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                                       gamma-3 heavy chain disease proteins - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
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Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: GDB:IGHG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                       A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human
(Species: Homo sapiens (man)
C;Becies: Homo sapiens (man)
C;Becies: Homo sapiens (man)
C;Becies: Homo sapiens (man)
C;Becies: Homo sapiens
C;Becession: A8.2511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511
A;Reference number: A23511
A;Reference number: A23511
A;Reference number: A33511
A;Reference number: A33511
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetion:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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Jeg gamma-3 chain C region, form LAT - human

Jeg gamma-3 chain C region, form LAT - human

Jeg gamma-3 chain C region, form LAT - human

Jeg gamma-3 chain C region, form LAT - human

C;Species: Homo sapiens (man)

C;Accession: A60764

R;Huck, S:, Lefranc, G:, Lefranc, M.P.

Immunogenetics 30, 250-257, 1989

A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an Jeg ference number: A60764; MUID:90007613; PMID:2571587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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225 QYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 524; DB 2; Length 377;
Pred. No. 3.6e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB.IGHG3
A;Cross-references: GDB.119339; OMIM.147120
A;Map position: 14q32.33-14q32.33
A;Introns: 94,3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin homology F;20-85/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 377;
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
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Pred. No. 3.6e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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91.5%;
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1 Similarity 91.5%;
97; Conservative
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Best Local Similarity
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
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Gaps

Ig gamma 2b chain constant region - pig (fragment)

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A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122 C;Genetics:
A;Gene: IgG1
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A;Molecule type: mRNA
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                     A; Accession: 147162
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                                                                                                                                                                         A; Residues:
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
R;Accession: 147166
B; Hacskovics, I:; Sun, J:; Butler, J.E.
J: Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Accession: 147160
A;Accession:
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Ig game 2a chain constant region - pig (fragment)
Ig games: Sus screfa domestica (domestic pig)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C; Date: 147159
Ignaminol: 147159
Immunol: 153, 3565-3573, 1994
Inmunol: 153, 3565-3573, 1994
In
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147162
Gigamma 4 chain constant region - pig (fragment)
Cj gamma 4 chain constant region - pig (fragment)
Cj gamma 5 corofa domestica (domestic pig)
Cj pate: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
Cj Accession: 147162
R; Kacskovics, I.; Sur, J.; Butler, J.E.
B; Kacskovics, I.; 3565-13573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences A; Reference number: 147158; MUD:95015845; PMID:7930579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 78.8%; Score 458; DB 2; Length 328; 1 Similarity 78.8%; Pred. No. 1e-37; 82; Conservative 14; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 328;
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C,Superfamily: immunoglobulin C region; immunoglobulin homology
F,133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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; Pred. No. 1e-37;
14; Mismatches 8;
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A;Molecule type: mRNA
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78.8%;
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Best Local Similarity
Matches 82; Conserva
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Best Local 9
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C;Accession: 147161
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A;Reference number: 147158; MUD:95015845; PMID:7930579
A;Accession: 147161
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K,Acskovics, I.; Sun, J.; Butler, J.B.
J. Immunol. 153, 3565-3573, 1994
A,Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A,Reference number: 147158; MUID:95015845; PMID:7930579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig gamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                   A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130 C;Genetics:
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C,Superfamily: immunoglobulin C region; immunoglobulin homology
F,82-151/Domain: immunoglobulin homology <IMM>
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F;133-202/Domain: immunoglobulin homology <IMM>
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76.1%; Score 442; DB 2;
Best Local Similarity 77.1%; Pred. No. 3.9e-36;
Matches 81; Conservative 13; Mismatches 11;
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
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A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
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Jeavy chain precursor (B/WT.4A.17.H5.A5) - bovine

Ig heavy chain precursor (B/WT.4A.17.H5.A5) - bovine

NyAlternate names: Ig gamma-1 chain C region (clone 8.10)

C;Speciaes: Boe primigenius taurus (cattle)

C;Date: 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S22080; S06610; Ā31303

R;Sanders P.G.

Submitted to the EMBL Data Library, November 1991

A;Reference number: S22080

A;Accession: S22080

A;Accession: S22080

A;Accession: S22080

A;Accession: S22080

A;Accession: Canary

A;Residues: 1-470 <SAN.>

A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440

R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.

Mol. Immunol. 26, 841-880, 1989

A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamm A;Reference number: S06610; MUD:90097956; PMID:2513487

A;Rocession: S0610

A;Rocession: Canary

A;Rocession: S0610

A;Rocession: Canary

A;Rocession: S0610

A;Rocession: Canary

A;Roces
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AjIntrons: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                           4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
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                                                                                                                                       Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 108
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                                                                                                                                                                                                                    11; Indels
                                                                                                                                   f; Score 442; DB 2;
f; Pred. No. 3.9e-36;
13; Mismatches 11;
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77.1%;
                                                                                                                          Query Match
Best Local Similarity 77.1%
Matches 81; Conservative
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524	520	504 443	420	413 410.5	410.5	410.5	396
32	3 8 E	36	8 6 6	40	4 4 2 6	44	45

ALIGNMENTS

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SECUENCE OF 2-326 FROM N.A.
MEDLINE=82197621; PubMed=6804948;
Blison J.W., Hood L.B.;
"Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant regine genes";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Fetal liver;
MEDLINE=8423592; PubMed=6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma "Comparison of the hinge-coding segments in human and the linkage of the gamma 2 and gamma 4 subclass heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal liver;
MEDLINE=83001943; PubMed=6811139; DOI=10.1016/0092-8674(82)90183-0;
Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
"Structure of human immunoglobulin gamma genes: implications for cevolution of a gene family.";
Cell 29:671-679(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
MEDLINE-80001357; PubMed=113060;
Connell G.E., Parr D.M., Hofmann T.;
The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";
Can. J. Biochem. 57:758-767(1979).
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SEQUENCE OF 238-275 (ZIE).
MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang A.-C., Tung E., Fudenberg H.H.;
"The primary structure of a human IgG2 heavy chain: genetic,
evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
               326 AA
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                                                                                                       Ig gamma-2 chain C region.
Name=IGHG2;
                 STANDARD;
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                                                                                                                                             Homo sapiens (Human)
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               HUMAN
GC2_HUMAN
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Local Similarity 93.6%;
nes 102; Conservative
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S -> A (in myeloma proteins TiL and ZIE).

FYTG=VAR, 003889.

C -> S (in Ref. 3).

8310878C6878CF9C CRC64;
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                                                                                                                                                                                  SEQUENCE OF 1-121 (DOT).

MEDLINE=95255298; PubMed=7737190;

Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri
"Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";

Eur. J. Biochem. 228:886-893(1995).
Hofmann T., Parr D.M.;
"A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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HSSP, P01857; 100X.
Genew; HGNC:526; IGHG2.
MIM; 147110; -.
GO:0005624; C:membrane fraction; NAS.
GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR00710; Ig-like.
InterPro; IPR00710; Ig-like.
InterPro; IPR007106; Ig_MHC.
Pfam; PF00047; Ig; 3.
PROSITE; PS00835; IG_LIKE; 3.
PROSITE; PS00299; IG_MHC; 2.
                                                                                                 REVISIONS TO 25; 59; 60 AND 264-268 (ZIE). Hofmann T., Parr D.M.; Submitted (MAR-1980) to the PIR data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=69064124; PubMed=5782707; Frangione B., Milestein C., Pink J.R.L.; "Structural studies of immunoglobulin G."; Nature 221:145-148(1969).
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CH2.
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MEDLINE=72033500, PubMed=4940472;
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DB 1; Length 326;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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THE German Human CDNA Consortium;

Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Fobo G., Han M., Wiemann S.;

Submitted (Aug-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640623; CAB45777.1;

HSSP; P01861; IADQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.4%; Score 554; DB 2; Length 41 Best Local Similarity 93.6%; Pred. No. 4.2e-46; Matches 102; Conservative 5; Mismatches 2; Indels
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 AA; 46061 MW; C4518E844CFB883C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686104196 (Fragment).
Name-DKFZp686104196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 3.2e-46;
5; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  465 AA
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InterPro; 1PR003109; 19.
InterPro; 1PR003100; 19-like.
InterPro; 1PR0031006; 19_MHC.
InterPro; 1PR003596; 19_WHC.
InterPro; 1PR003596; 19_WHC.
InterPro; 1PR003596; 10_WHC.
InterPro; 1PR003596; 10_WHC.
InterPro; 1PR003590; 1PR0035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Q6P6C4;
05-JUL-2004 (TrEMBLrel).
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NON_TER 1
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266664
1D 06666
DAC 06666
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1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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C TISSUER ectum tumor;

The German cDNA Consortium;

A Bloccker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,

A Osanger A., Fobo G., Han M., Wiemann S.;

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; CR748861; CR41870511; ---

R InterPro; IPR0031599; Ig. 1.

R InterPro; IPR0031597; Ig. 1.

InterPro; IPR0031597; Ig. 1.

R InterPro; IPR0031597; Ig. 1.

R Pfam; PF07654; Cl. set; 3.

R Pfam; PF07654; Cl. set; 3.

R SMART; SM00407; IG. 1.

R SMART; SM00406; IG. 1.

R SMART; SM00406; IG.; 1.
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
4. Last annotation update)
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4. Last annotation update)
6. Last annotation update)
6. Last annotation update)
6. Last annotation (Translate)
6. Last annotation (Last annotation)
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SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493 AA; 54117 MW; A1E4F5ED3FA8AB40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.8%; Score 551; DB 2; L6
92.7%; Pred. No. 9.3e-46;
Mismatches 2;
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PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN_2.
                            TISSUE-Human rectum tumor;
The German Human cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 101; Conservative
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        SEQUENCE FROM N.A.
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Q68CN4
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                                                                                                                        Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rownstein M.J., Usdin T.B., Toodhiyuki S., Carninci P., Prange C., A Broask S.A., McKenan K.J., Malek J.A., Gubbs N.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahery J., Helton B., Ketteman M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G., A Norieskon M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Scherztion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
[1]
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0
                                                                           TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 554; DB 2; Length 46:
Pred. No. 4.7e-46;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC062335; AAH62335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS0290; IG_MHC; UNKNOWN_2.
HYPOCHELICAL protein_
SEQUENCE 465 AA, 51325 MW; FDDB9348ADC37E6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Name=DKFZp686C15213;
Homo sapieng (Human).
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_N-
Pfam; PP07654; C1-set; 3.
SWART; SW004007; IGC1; 3.
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93.6%;
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nes 102; Conservative
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                                                  SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
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Schwarz J., Reichel W., Hilschmann N.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE (MYELOMA PROTEIN NIE).
MEDLINES-77070569; Dubade=826475;
Ponstingl H., Hilschmann N.,
"The rule of antibody structure. The primary structure of a monoclonal igg1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
                                 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).

MEDLINE=71064024; PubMed=5489771;

Cunnipham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,

Maxdal M.J., Edelman G.M.;

"The covalent structure of a human gamma G-immunoglobulin. VII. Amino
acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
              Gaps
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                                                                                                                                                                                                                                                                                                            Ellison J.W., Berson B.J., Hood L.E.; "The nucleotide sequence of a human immunoglobulin C gammal gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
MEDLINE=83289131; PubMed=6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. 8. Ami acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; Biochemistry 9:3171-3181(1970).
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                                                                                       61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 136-329 (EU).
MEDLINE=71064025; PubMed=5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
            4; Indels
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  Pred. No. 3.9e-45;
                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                       330 AA
             5; Mismatches
                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 10:4071-4079(1982).
                                                                                                                                                       PRT;
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DISULFIDE BONDS.
MEDLINE=77070267; PubMed=1002129;
                                                                                                                                                                                                                                                                                      GEQUENCE FROM N.A.
MEDLINE=82274238; Pubmed=6287432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=71064027; PubMed=4923144; Gall W.E., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry 9:3188-3196(1970)
91.78;
                                                                                                                                                                                                            gamma-1 chain C region
             100; Conservative
                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                 Homo sapiens (Human)
  Best Local Similarity
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                                                                                                                                                                                                                        Name=IGHG1;
                                                                                                                                                       GC1_HUMAN
P01857;
                                                                                                 338
             Matches
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                                                                                                                                                                                                                                                                                                                                  Biochemistry 20:2361-2370(1981)...;
Biochemistry 20:2361-2370(1981)...;
In MISCELLANBOUS: Nie has the GiM(17) allotypic marker, 97-K, and the GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the GIM(3) marker and the GIM (non-1) markers.

IIS, 188, 269 and 272...

MISCELLANBOUS: EU also differs in the amidation states of 35, 116, 198, 269 and 272...

ISS, 166, 177, 195, 198, 269, and 272 and in the order of residues 268-272...
                                                                                                                                                                                                                                                                     "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";
"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- MISCELLANEOUS: KOL also differs in the amidation states of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain).
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(with heavy chain)
(with heavy chain)
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NOW TER 1 1 98 CH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005624; C:membrane fraction; NAS. GO:0003823; F:antigen binding; TAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interchain (
Interchain (
Interchain (
                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
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Hinge.
CH2.
CH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; J002228; AAC82527.1; ALT_INIT.
A93433; GHHU.
                                                                                                                                                                                                             MEDLINE=81208100; PubMed=7236608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; 1D51; ...ray; n--
PDB; 1D67; X-ray; n--
PDB; 1DN2; X-ray; A/B=120-320.
RPB; 1EC1; X-ray; A/B=106-329.
DR PDB; 1FC2; X-ray; A/B=106-329.
DR PDB; 1FC2; X-ray; D=106-329.
DR PDB; 1FC2; X-ray; D=106-329.
DR PDB; 1FC2; X-ray; A=121-326.
DR PDB; 1172; X-ray; A/B=107-330.
TTC; X-ray; A/B=107-330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUB; IFC1; X-ray; M, M=106-329.
PDB; IFC2; X-ray; D=106-329.
PDB; IFC2; X-ray; D=106-329.
PDB; ITC2; X-ray; B, D=1-136.
PDB; IITZ; X-ray; B/D=1-103.
PDB; IITZ; X-ray; B/D=1-103.
PDB; IITS; X-ray; A/B=107-330.
PDB; IICX; X-ray; A/B=107-330.
PDB; IOQX; X-ray; A/B=119-330.
PDB; ZRCS; X-ray; H=1-103.
Genew; HGNC:5525; IGHG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residues 198, 267 and 272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00047, ig, 3.
PROSITE, PS50835; IG LIKE; 3.
PROSITE, PS00290; IG MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B/H=1-101.
H=1-101.
H=1-101.
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223
330
83
103
1112
204
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1D5B; X-ray;
                                                                                                                                                                                                                                            Deisenhofer J.;
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2 PP-----VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
93.5%; Score 543; DB 2; Length 34
Best Local Similarity 90.4%; Pred. No. 4.2e-45;
Matches 103; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                        Zhu N.S., Chen Y.Y.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS70731, AAS88328.1; --
HSSP; P01857; 1AJ7.
                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hepatitis B virus receptor binding protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 348 AA; 38162 MW; DD96C3D7E0BE5845 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                GO, GO:0004872; F:receptor activity; IEA. InterPro; IPR007110; Ig-like. InterPro; IPR003507; Ig-c1. InterPro; IPR003506; Ig-MHC. Pfam; PF07654; C1-set; 3. SMART; SMO407; IGC1; 3. PROSITE; PS00825; IG_LIKE; 3. PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                   NCBI_TaxID=9606;
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Q6GMX6
                                           STANDORRAN SERVICE SOCIAL SERVICE SERVICE SOCIAL SERVICE SOCIAL SERVICE SERV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                N-linked (GlcNAc. .).
K -> R (in GlW(13) marker).
KTIGWVAR 003886.
D -> E (in GlM(non-1) marker).
FTIGWORR 003887.
L -> M (in GlM(non-1) marker).
/FTIG=VAR_003889.
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Best Local Similarity 90.4
Matches 103; Conservative
308
180
97
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164
167
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5

TISSUB-Primary B-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straueberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Butchew K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

B Altschul S.F., Lordan H., Porner T.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

110 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN

AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109

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Matches 103;
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Q7Z7P5;
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Marby D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.B., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ratealey R.W., Touchman J.W., Green B.D., Dickson M.C.,

Ratiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smallus D.B., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                 Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PP-----VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKTKPREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
9
                                                                                                                                                                                                                                              Straubberg R.;
Submitted (UUN 2004) to the EMBL/GenBank/DDBJ databases.
Submitted (UUN 2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC073766, AAH7766.1;
InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003066; Ig.
R Pfam; PP00047; Ig. 4.
SWART; SW00409; IG; 2.
SWART; SW00406; IGv; 1.
R PROSITE; PS50835; IG_LIKE; 4.
R PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.5%; Score 543; DB 2; Length 465; Best Local Similarity 90.4%; Pred. No. 5.7e-45; Matches 103; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                      PISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein
SEQUENCE 465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
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                                                                                                                                                                                        SEQUENCE FROM N.A.
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Name=IGHG1;
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Klausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausherg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
An staleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia S., Sanchez A.M.
Richards S., Worley K.C., Hale S., Garcia C.S., Shevchenko Y., Boulfard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.J.,
Jones S.J., Marra M.J.,
Jones S.J., Marra M.J.,
Jones S.J., Marra M.J.,
Jones S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 305
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'Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO01359; Ig.
InterPro; IPR00359; Ig.
InterPro; IPR003509; Ig-like.
InterPro; IPR003006; Ig-like.
InterPro; IPR003006; Ig-like.
InterPro; IPR003596; Ig-u.
InterPro; IPR00409; Ig-u.
INTERPOSITE; IPR00409; IRR00409; IRR00409;
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TISSUE=Peripheral Nervous System;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072419; AAH72419.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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llarity 90.4%; Pred. No. 5.7e-45;
Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 AA
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                                                                          CDNA
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Q7Z5W1;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Collins F.S., Mangner L., Shenmen C.M., Schuler G.D.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenco M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Pahey J., Helton E., Ketteman M., Madan A.M., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Iakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

M RIXYMIBKI M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PP-----VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 362
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                             93.5%; Score 543; DB 2; Length 469; 90.4%; Pred. No. 5.8e-45; ive 2; Mismatches 3; Indels
                                               Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO51328; AAH51328.1; -.
HSSP; P01857; 1HZH.
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Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                            PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last sequence update) C-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein. Homo sapiens (Human).
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                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR003066; Ig WHC.
InterPro; IPR003596; Ig V.
Pfam; PF07654; C1-set; 3.
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HSSP; P01861; 1ADQ.
InterPro; IPR003599; IG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                           SMART; SM00406; IGV;
SEQUENCE FROM N.A.
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066744
10 66744
AC 06674A
AC 06674A
AC 06674A
DT 05-JUU
DE HYDOT
OC BURAR
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RA ALIASS
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Attaubnes_2188257; Pubmed=144,792; DOI=10.10.5/pnas.44203059;
A Straubberg R.L., Feingold E.A., Groues L.H., Dorge J.G.,
Altschul S.P., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.P., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A stapleton M. Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tonshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
Richards S., Worley K.C., Hale S., Garcia S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PP-----VAGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFWWYVDGVEVHN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
מיזייי בייייי איזיירי איזיירי
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 470;
InterPro; IPR003110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003066; Ig_WHC.
InterPro; IPR003066; Ig_V.
Pfam; PF07654; C1-set; 3.
SWART; SW00409; IG6, 2.
SWART; SW00406; IGV; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 470 AA; 51715 MW; 7B49556AllFD7D99 CRC64;
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053984; AAH53984.1; -.
HSSP; P01857; 1HZH.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Homo sepiens (Human).
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 93.5%; Score 543; DB 2; L
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 AA.
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Interpro; IPR003597; Ig cl.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
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Q6P055
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Q6P055
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                                                                                                                                                                                                                                                                  252 PPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 311
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                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                     56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                 56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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9
                                                                                                                                                                      Query Match 93.5%; Score 543; DB 2; Length 470; Best Local Similarity 90.4%; Pred. No. 5.8e-45; Matches 103; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.5%; Score 543; DB 2; Length 472; 90.4%; Pred. No. 5.8e-45; live 2; Mismatches 3; Indels
                                                                                            Hypothetical protein.
SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51724 MW; 26CB340D0046D279 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...wublrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686P15220.
Homo sapient (Treatment of the content of the conten
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InterPro; IPR003599; IG.
InterPro; IPR003597; IG_C1.
InterPro; IPR003597; IG_MHC.
InterPro; IPR003596; IG_WHC.
InterPro; IPR003596; IG_WHC.
InterPro; IPR003596; IG_WHC.
InterPro; IPR003596; IG_WHC.
INTERPRO; IRR0409; IG, 2.
SWART; SW00400; IGY; 1.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00835; IG_LIKE; 4.
                    SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Human rectum tumor;
The German Human cDNA Consortium;
  Pfam; PF07654; C1-set; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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SEQUENCE 472 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q6N089
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Q6N089
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PRELIMINARY;

O6MZV7;

RESULT 14 Q6MZV7 ID Q6 AC Q6

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253 PPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 312
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TISSUB-Peripheral Nervous System;

TISSUB-Peripheral Nervous System;

MEDLINE-2238825; PubMed-12477932; DOI=10.1073/pnas.242603899;

Katausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heibh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                       A Liberberghulant burner contributed of The German Human convactions;

The German Human convactions;

A Fobo G., Han M., Wiemann S.;

L Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

E MBL; BK640833; CA645920.1; -..

R EMBL; BK640833; CA645920.1; -..

R InterPro: IPR003599; Ig. C1.

R RART; SM00409; IG; 2.

R SWART; SM00409; IG; 2.

R SWART; SM00406; IGV; 1.

R PROSITE; PS050835; IG_LIKE; 4.

R PROSITE; PS050835; IG_LIKE; 4.

R PROSITE; PS050835; IG_LIKE; 4.

R PROSITE; PS050835; IG_LIKE; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEOUENCE 473 AA; 52121 MW; 9476EAE4COBFC447 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686Cil1235.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo seaplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
93.5%; Score 543; DB 2;
Best Local Similarity 90.4%; Pred. No. 5.8e-45;
Matches 103; Conservative 2; Mismatches 3.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Human small intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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9
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C TISSUE-Peripheral Nervous System;
A Strausberg R.;
A Strausberg R.;
B Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
R BMBL; BC065820; AAH65820.1; -.
R HSPS; P01861; JADO.
R InterPro; IPR001599; Ig-1ike.
R InterPro; IPR001599; Ig-1ike.
R InterPro; IPR001599; Ig-21.
R InterPro; IPR001596; Ig-MHC.
R InterPro; IPR001596; Ig-MHC.
R SMART; SM00409; IG-1: 3.
R SMART; SM00409; IG-1: 3.
R SMART; SM00409; IG-1: 1G-1: 3.
R SMART; SM00409; IG-1: 1G-1: 3.
R SMART; SM00409; IG-1: IG-1: 3.
R PROSITE; PS508299; IG-1/RKE; 4.
R PROSITE; PS00209; IG-MHC; UNKNOWN_2.
HYPOCHELICAL PFOCEE:
W HYPOCHELICAL PFOCEE:
W HYPOCHELICAL PROCEE:
W SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;
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Pred. No. 5.8e-45;
2; Mismatches 3;
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Best Local Similarity 90.4%;
Matches 103; Conservative
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Search-completed: November 17, 2005, 07:10:19 Job time : 81.8836 secs

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Sequence 18, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 5, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 63, Appli
Sequence 28, Appli
Sequence 32, Appli
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                                                                                                                                                                   1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKAK 109
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-444-644-30

US-09-433-588-5-30

US-09-433-588-5-7

US-09-968-362A-27

US-08-379-516-2

US-08-379-516-2

US-09-329-916-2

US-09-329-916-2

US-09-472-087-2

US-09-766-995-2

US-09-766-995-2

US-09-76-087-10

US-09-472-087-10

US-09-473-087-10

US-09-859-053-36

US-09-859-053-36

US-08-372-36-4
                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                 November 17, 2005, 06:51:22
                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                       US-09-674-857-1
581
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Perfect score:
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No.
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						ALIGNMENTS	
·	RESULT 1 US-09-968-362A-18 Sequence 18, Ap Patent No. 6797 GENERAL INFORMA APPLICANT: Su CURRENT FILING CURRENT FILING NUMBER OF SEQ CURRENT APPLIC CURRENT APPRIC CURRENT APPRIC CURRENT APPRIC CURRENT APPRIC CURRENT APPRIC CURRENT APPRICANT CURRENT APPRICANT CORPER INFORMA US-09-968-362A-18	ULT 1 09-968-362A-18 equence 18, Ap atent No. 6797 atent No. 6797 APPLICANT: Sun APPLICA	SULT 1 -09-968-362A-18 Patent No. 6797493 GENERAL INFORMATION: APPLICANT: Sun, Lee-Hwei: APPLICANT: Sun, Bill APPLICANT: Sun, Eccily R TITLE OF INVENTION: Incr FILE OF INVENTION: Incr FILE OF INVENTION: Incr FILE OF INVENTION: Ec fu FILE SEFERENCE: 035002001 CURRENT APPLICATION NUMBE: CURRENT APPLICATION NUMBE: CURRENT APPLICATION NUMBE: CURRENT APPLICATION NUMBE: LENGTH: 448 TYPE: PRT COFFER INFORMATION: ACT OTHER ACT OTHER INFORMATION: ACT OTH	ULT 1 109-968-362A-18 109-968-362A-18	/09 ion asse -10 -10 -1.	proteins of human gripological activition of 1/09/968,362A	ranulocyte colony-stimulaing factor ies -amino acid leader peptide (Figure
	Query M Best Lo Matches	atch cal	į	96.2% larity 94.5% Conservative	50 to	Score 559; DB 4; Pred. No. 4e-56; 5; Mismatches 1;	Length 448; Indels 0; Gaps 0;
····	o oo	233 61 61 293	APPVAGP APPVAGP REEQYNS' 	PVAGPSVFLFPPKPI 	PKO PKO PKO PKO PKO PKO PKO PKO PKO PKO		CUVUDUSHEDPEVKFNWYVDGVEVHNAKTKP 60
	RESULT 2 US-08-444-644-30 Sequence 30, A Patent No. 601 GENERAL INFOR TITLE OF IN	17 2 1444-644-30 1444-644-30 140ence 30, Applicant No. 601555 18EAL INFORMATICANT: Fri TITLE OF INVENT: TITLE OF INVENT: TITLE OF SQUENTESPONDENCE 1 ADDRESSEE: HADDRESSEE: HA	ULT 2 08-444-644-30 atence 30, Application atent No. 601555 GENERAL INFORMATION: APPLICANT: Friden, Ph TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF SEQUENCES: CORRESPONDENCE ADDRESS ADDRESSEE: Hamilton STREET: Two Milltia	ion SS: SESS	JS/084 TILLIP RANSFE WTIBOD NUUGA 46 : Broo	RECEPTOR SPECIFI UROPHARMACEUTICAL mith & Reynolds,	C OR DIAGNOSTIC AGENT

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RESULT 4
US-02-483-588-5
'Sequence 5, Application US/09483588
'Patent No. 6737056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 109 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-232-246A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-08-232-246A-30
US-08-232-246A-30
Sequence 30, Application US/08232246A
Patent No. 6329508
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF INVENTION: CONJUGATES
NUMBER OF REQUIRES: 46
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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Pred. No. 2.4e-56;
5; Mismatches 2; Indels
                                                                                                                                 OPERATING SYSTEM: PC-DOS/MO-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                       APPLICATION NOTICE TO THE PELLING DATE:
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
RIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
NAME: Wagner, Richard W.
REFERENCE/DOCKET NUMBER: 34/480
REFERENCE/DOCKET NUMBER: 34/480
REFERENCE (617) 861-6240
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
ITPER: amino acids
TOPOLOGY: linear
                                                                                               3: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 93.6%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STREET: Two Mili
CITY: Lexington
STATE: MA
COUNTRY: USA
Lexington
                                    USA
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1 APPVAGPSVFLFPPKRDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: POLYPeptide Variants with Altered Effector Function
FILE REFERENCE: P1726f1
CURRENT APPLICATION NUMBER: US/09/483,588
CURRENT APPLICATION NUMBER: US 60/116,023
EARLIER APPLICATION NUMBER: 1999-01-15
SARLIER FILING DATE: 1999-01-15
SEQ ID NOS: 11
ERGITH: 217
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURSOT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
95.4%; Score 554; DB 3;
Best Local Similarity 93.6%; Pred. No. 2.4e-56;
Matches 102; Conservative 5; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPERRNCE/POCKET NUMBER: 34,480
REPERRNCE/POCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acida
                                                                APPLICATION NUMBER: US/08/232,246A FILING DATE: 04-MAY-1994 CLASSIPICATION 530 FRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/800,458 FILING DATE: 26-MOV-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/US90/05077 FILING DATE: 07-SEP-1990 PRIOR APPLICATION NUMBER: US 07/404,089 FILING DATE: 07-SEP-1989 ATTORNEY/AGENT INPORMATION: NAMME: WAGNEY, RICHARD NUMBER: 34,480
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Query Match
Best Local Similarity 93.6%;
Matches 102; Conservative
                                                                   LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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Matches 102; Conservative
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SEQ ID NO 2
    TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           ORGANISM: homo sapien
                                                                                                                                                                                                                                CELL TYPE: lymphocyte
                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                              Sequence 27, Application US/09968362A
Patent No. 6797493
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sun, Bill
APPLICANT: Sun, Cecily R
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: For fusion proteins of human granulocyte colony-stimulaing factor TITLE OF INVENTION: Proceased biological activities
FILE REFERENCE: 03SUN2001
CURRENT APPLICATION NUMBER: US/09/968,362A
CURRENT APPLICATION DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INPORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 72
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62 REBQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Human 1gG2 Fc with native hinge, CH2 and CH3 domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 554; DB 4; Length 228;
Pred. No. 6.3e-56;
5; Mismatches 2; Indels
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SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,460B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTONEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPM/AJM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 93.6
Matches 102; Conservative
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                US-09-968-362A-27
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US-08-477-460B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 27
LENGTH: 228
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Sequence 2, Application US/08379516

Sequence 2, Application US/08379516

Sequence 2, Application US/08379516

Sequence 2, Application US/08379516

GENERAL INFORMATION:
APPLICANT: Allaway, Graham P.
APPLICANT: Allaway, Graham P.
TITLE OF INVENTION: Immunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
CURRENT APPLICATION NUMBER: US/08/379,516
CURRENT PILING DATE: 1996-06-10
EARLIER FILING DATE: 1995-08-06
EARLIER FILING DATE: 1992-08-06
EARLIER FILING DATE: 1992-08-07
NUMBER: OF CONTENT OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-329-116-2
US-09-329-16-2
Sequence 2, Application US/09329916
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
UNMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   217 APPVAGPSVFLFPPRKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
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                                                                                                                                                                                                                                   1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                          Gaps
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95.4%; Score 554; DB 3; Length 432; 93.6%; Pred. No. 1.4e-55;
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                                                                                                                    2; Indels
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Pred. No. 1.4e-55;
5; Mismatches 2;
                                                                                                                    5; Mismatches
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PatentIn Release #1.24
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 412
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 472 amino acids TYPE: amino acid STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL TYPE: lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10112
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-485-372A-2
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Pred. No. 1.4e-55;
5; Mismatches 2; Indels
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US-08-485-372A-2
i Sequence 2, Application US/08485372A
i Patent No. 6187748
i GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 1
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
COUNTRY: New York
STATE: New York
COUNTRY: USA
                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: Datentin Release #1.24

COMPUTER: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/329,916

FILING DATE:

CLASSIFICATION DATA:

APPLICATION NUMBER: 08/477,460

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: 08 07/927,931

FILING DATE: 07-JUN-1992

APPLICATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

TELECHONE: (212) 977-9809

TELECHONE: (212) 977-9809

TELESA 422523 COOP ITELESTICES:

TENDRATION FOR SEQ ID NO: 2:

SCOUNCE CHARACTERISTICS:

TENDRATION FOR SEQ ID NO: 2:

SCOUNCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
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Best Local Similarity 93.6%;
Matches 102; Conservative
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TYPE: amino acid
STRANDEDNESS: unknown
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CELL TYPE: lymphocyte
US-09-329-916-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                         New York
: New York
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                                           CITY: New
STATE: Ne
COUNTRY:
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Sequence 2, Application US/09409006A
Patent No. 6342586
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVHNAKTKP 276
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,372A
FILING DATE:
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,227
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-A
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: ELOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409, 006A
FILING DATE: 29-SEP-1999
CLASSIFICATION A24
PRIOR APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
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1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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Patent No. 6453313

GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
ITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTY

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,681
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-B
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEFAX: (212) 391-0525
                   TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.6
Matches 102; Conservative
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                                                                                                                                                                               unknown
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; CELL TYPE: lymphocyte
US-08-484-681-2
                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                       ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                 CELL TYPE: lymphocyte
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                unknown
                                                                                                                                                        TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                  US-09-409-006A-2
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US-08-484-681-2
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Patent No. 6737267
GENERAL INFORMATION:
APPLICANT: GTADAM P. Allaway et al.
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 2048/41215-CB/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/766,995
CURRENT FILING DATE: 2011-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
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GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: ONN-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                         217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
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                                                                                   1 APPVAGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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    Length 432;
Score 554; DB 4; Length 43
Pred. No. 1.4e-55;
5; Mismatches 2; Indels
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ZIP: 10112
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
  Query Match
Best Local Similarity 93.6%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: 07-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: homo sapians
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 30 Rocket
CITY: New York
STATE: New York
COUNTRY: USA
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US-09-766-995-2
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US-09-472-087-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 APPVAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APPVAGPSVFLFPPKPKDTLMISRIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
95.4%; Score 554; DB 5; Length 432;
Best Local Similarity 93.6%; Pred. No. 1.4e-55;
Matches 102; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REPRENCE: ABX-PBLICANION NUMBER: US/09/472,087
CURRENT APPLICANION NUMBER: US/09/472,087
            NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 41215-A-PCT/JPW/AJM
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPA: 422523 COOP UI
TELEPA: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 70, Application US/09472087
Patent No. 6682736
                                                                                                                                                                                                                             LENGTH: 432 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
PCT-US93-07422-2
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 93.6
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-472-087-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-472-087-70
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RESULT 15

Appl Appl

Sequence 1 Sequence 5 Sequence 5 Sequence 5 Sequence 5 Sequence 3

Sequence Seq

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Length 329;

Score :

100.0%;

Query Match Best Local Similarity

581 573 567 567 567 567 567 567 57

Score

Result 80

Sequence 3, Sequence 3, Sequence 74

Sequence

Sequence Seq

Perfect score:

. Н

Sequence:

Scoring table:

Searched:

Database

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581; DB 20;
No. 1.1e-48;
3 US-10-959-318-16

US-09-925-218-18

US-10-16-518A-18

US-11-016-518A-18

US-10-968-3162-18

US-10-800-497-18

US-10-800-497-18

US-10-800-497-18

US-10-959-318-2

US-10-959-318-2

US-10-959-318-2

US-10-959-318-2

US-10-959-318-2

US-10-959-318-2

US-10-968-3-3

US-10-968-3-3

US-10-982-470-5

US-10-684-109-75

US-10-684-109-75

US-10-047-542-2

US-10-047-542-2

US-10-047-542-2

US-10-047-542-2

US-10-047-542-2

US-10-047-542-2

US-10-047-544-2

US-10-075-448-2

US-10-928-305-378-37
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APPLICANT: KLING, DORCTHEE
APPLICANT: KOPETZKI, ERHARD
APPLICANT: REBERS, FRANK
APPLICANT: STENNE, PAUL
APPLICANT: STENNE, BEAT
APPLICANT: STENNE, ANNE
APPLICANT: STENEN, ANNE
APPLICANT: STREIN, PAMELA
APPLICANT: STUBENRAUCH, KAY-GUNNAR
APPLICANT: VAN DE WINKELA, JAN
APPLICANT: VAN DE WINKELA
TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
FILE REFERENCE: 22354
CURRENT APPLICATION NUMBER: US/11/102, 403
PRIOR APPLICATION NUMBER: EP 04008722.3
PRIOR APPLICATION NUMBER: EP 04008722.3
PRIOR PILING DATE: 2004-04-13
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PALENTIN VET: 3.3
SEQ ID NO 25
LENGTH: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIRANDA
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Publication No. US20050226876A1
GENERAL INFORMATION:
                                              APPLICANT: GRAUS, YVO
APPLICANT: HIWBER, JACQUES
APPLICANT: JANSEN-WOLENAAR,
APPLICANT: KLING, DOROTHEE
APPLICANT: KOPETZKI, ERHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-403-25
    JS-11-102-403-25
    \( \text{R} \) \( \te
      11, Appl
12, Appl
11, Appl
67, Appl
67, Appl
9, Appl
16, Appl
16, Appl
15, Appl
                                                                                                                                        ; Search time 83.6164 Seconds
(without alignments)
545.427 Million cell updates/sec
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Sequence 12, 2
Sequence 11, 3
Sequence 67, 3
Sequence 67, 3
Sequence 67, 3
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                                                                                                                                                                                                                                                              1 APPVAGPSVFLFPPKPKDTL.....CKVSNKGLPSSIEKTISKAK 109
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/NS06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/NS06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/NS08_NEW_PUB.pep:*
7/cgn2_6/ptodata/1/pubpaa/NS08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/NS08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                             1867879
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-959-318-11
US-10-959-318-12
US-10-493-676-11
US-10-307-724-67
US-10-307-724-67
US-10-959-318-9
US-10-959-318-10
US-10-745-775-16
US-10-745-775-16
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                                                                                                                                                                                                                                                                                                                                                            1867879 segs, 418409474 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                          November 17, 2005, 07:05:08
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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94.6
97.2
97.2
96.8
96.8
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Match
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Gaps

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Gaps

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0; Indels

0; Mismatches

Matches 109; Conservative

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216 APPVAGPSVFLFPFRPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 275
                                                                                                                                                     1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                1 APPVAGPSVFLFPPKPKDTLMISRIPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTKP
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                                                               Length 109;
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Publication No. US20030049683A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REPERENCE: 1087-2
CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-12-05
PRIOR FILING DATE: 2000-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.6%; Score 567; DB 16;
97.2%; Pred. No. 3.6e-47;
cive 1; Mismatches 2;
                                                               Score 573; DB 18;
Pred. No. 1.9e-48;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: FD1D2-Igatp
                                                               Query Match
Best Local Similarity 99.1%;
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
; OTHER INFORMATION: mutations US-10-959-318-12
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Matches 106; Conservative
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US-10-006-593-67
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US-10-959-318-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and e (E268)
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                                                                                     114 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 173
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                                                                                                                                                                                                                                                      US-10-959-318-11

Sequence 11, Application US/10959318

Sequence 11, Application US/10959318

Publication No. US2000215768A1

GENERAL INFORMATION:
APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TTLLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302
CURRENT FILING DATE: 2004-10-07

PRIOR APPLICATION NUMBER: US/10-07

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 11

LENGTH: 109
                                             1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REPERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR PILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: G80324368.0
PRIOR FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.3
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                                                                                                                                61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                            174 REEQYNSTYRUVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 98.6%; Score 573; DB 18; Length 109; Best Local Similarity 99.1%; Pred. No. 1.9e-48; Matches 108; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 12, Application US/10959318; Publication No. US20050215768A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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US-10-959-318-12
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LENGTH: 109
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Gaps

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Publication No. US20040253242A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.2%; Score 565; DB 14; Length 472; Best Local Similarity 97.2%; Pred. No. 6.1e-47; Matches 106; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renehaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2cip
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-39
PRIOR FILING DATE: 2001-05-39
PRIOR FILING DATE: 2001-05-39
PRIOR FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 134
                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Humanized antibody heavy chain
US-10-006-593-67
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97.2%; Score 565; DB 15;
Best Local Similarity 97.2%; Pred. No. 6.1e-47;
Matches 106; Conservative 2; Mismatches 1;
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PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR PELING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 67
LENGTH: 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 67, Application US/10307724; Publication No. US20030232972A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: artificial sequence
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US-10-737-290-67
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; Sequence 67, Application US/10737290

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; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and d (D268); OTHER INFORMATION: mutations
US-10-959-318-9
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Supplication NO. US2005215768A1

SUBDILICATION NO. US2005215768A1

GENERAL INFORMATION:

APPLICANT: Armour, Kathryn L

APPLICANT: Clark, Michael R

TITLE OF INVENTION: Polypeptides including modified constant regions

FILE REFERENCE: 39-302

CURRENT APPLICATION NUMBER: US/10/959,318

CURRENT PILING DATE: 2004-10-07

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PARENTIN VERSION 3.3

SOFTWARE: PARENTIN VERSION 3.3
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APPLICANT: Evederickson, Shana
APPLICANT: Renshaw, Mark
APPLICANT: Renshaw, Mark
APPLICANT: Renshaw, Mark
APPLICANT: Ornoria, Cocilia
ITILE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REPERENCE: 1087-2 CIP III
CURRENT PAPLICATION NUMBER: US/10/737,290
CURRENT PLING DATE: 2003-12-15
PRIOR PILING DATE: 2003-06-02
PRIOR PILING DATE: 2003-06-02
PRIOR PILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR PILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-05-04
PRIOR PILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 193
SOFTWARE: Patentin version 3.2
SEQ ID NO 6: 472
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Pred. No. 2e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.2%; Score 565; DB 16;
97.2%; Pred. No. 6.1e-47;
tive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Humanized antibody heavy chain
US-10-737-290-67
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: artificial sequence
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Best Local Similarity 97.21
Matches 106; Conservative
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Best Local Similarity
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Gaps

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; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b and d (D268); OTHER INFORMATION: mutations
US-10-959-318-15
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                                                                                                                                                                                                                                                                                                                                                                                                                  1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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Sequence 15, Application US/10959318

Sequence 15, Application US/10959318

Publication No. US20050215768A1

GENERAL INFORMATION:
APPLICANT: Armour, Kathryn L

APPLICANT: Clark, Michael R

TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302

CURRENT FILING DATE: 2004-10-07

PRIOR APPLICATION NUMBER: PCT/GB2004/004254

PRIOR APPLICATION NUMBER: GB0324368.0

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 15

LENGTH: 109
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APPLICANT: Armour, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302
CURRENC APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR PELICATION NUMBER: PCT/GB2004/004254
PRIOR FILING DATE: 2004-10-07
PRIOR APPLICATION UNDRER: GB0324368.0
PRIOR PLING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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                                                                                                                                                                                                                                  Score 562; DB 16; Length 447;
Pred. No. 1.1e-46;
4; Mismatches 1; Indels
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                                                                                                     OTHER INFORMATION: Synthetic Construct
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Publication No. US20050215768A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.4%;
Matches 104; Conservative
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Best Local Similarity 96.3
Matches 105, Conservative
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                                                                                            1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
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             1; Gaps
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APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 304-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT APPLICATION NUMBER: PCT/GB2004/004254
PRIOR FILING DATE: 2004-10-07
PRIOR PILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: GB0324368.0
NUMBER OF SEQ ID NOS: 27
SOFTHARE: PALENCE AND NOS: 27
SOFTHARE: AND NOS: 27
SOFTHARE: AND NOS: 27
SOFTHARE: A PALENCE AND NOS: 27
SOFTHARE A
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                                                                                                                                                                                                                                                                                                                 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Pred. No. 2e-47;
0; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-10-745-775-16

Sequence 16, Application US/10745775

Publication No. US20040237124A1

GENERAL INFORMATION:
APPLICANT: POOSE, Jaume
APPLICANT: ROSENTHAL, ALTON
TITLE OF INVENTION: SAME
FILE REFERENCE: 514712001400
CURRENT APPLICATION NUMBER: US/10/745,775
CURRENT FILING DATE: 2003-12-24
PRIOR APPLICATION NUMBER: US 60/436,905
PRIOR APPLICATION NUMBER: US 60/435,22
PRIOR APPLICATION NUMBER: US 60/443,522
PRIOR APPLICATION NUMBER: US 60/410,006
PRIOR FILING DATE: 2003-10-28

PRIOR FILING DATE: 2003-10-08

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FESSES for Windows Version 4.0

LENGTH: 447

TWOE: DATE: DATE
             1; Indels
         0; Mismatches
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. Sequence 10. Application US/10959318
. Publication No. US20050215768A1
. GENERAL INFORMATION:
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         Matches 108; Conservative
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Best Local Similarity
Matches 108; Conserva
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LENGTH: 110
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Gaps

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OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure OTHER INFORMATION: 2A)
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OTHER INFORMATION: HuEPO-L-VFC gamma2 with a 27-amino acid leader peptide (Figure), OTHER INFORMATION: 2A)
US-11-016-518A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ### Sequence 18.7 Application US/11016518A

### Publication No. US20050124045A1

### GENERAL INFORMATION:

### APPLICANT: Sun, Lee-Hwei K

### APPLICANT: Sun, Cecily R

### TITLE OF INVENTION: For fusion proteins of human erythropoietin with increased

### TITLE OF INVENTION: Pological activities

### TITLE OF INVENTION: biological activities

### TITL
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Job time : 84.6164 secs
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 436
TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 103; Conservative
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US-11-016-518A-18
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Sequence 18, Application US/09912812
Sequence 18, Application US/09912812
Sequence 18, No. US20030082749A1
Sequence 18, No. US20030082749A1
GENERAL INFORMATION:
APPLICANT: Sun, Dell N
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biologi
FILE REFERENCE: 025UN2001
CURRENT APPLICATION UNMERE: US/09/932,812
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
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Sequence 18, Application US/10761593A
Sequence 18, Application US/10761593A
PUBLICATION NO. US20040175824A1
SERIERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Rc fusion proteins of human erythropoietin with high biological
TITLE OF INVENTION: activities
                                                                                                                                                                    PEATURE:
OTHER INFORMATION: Variant of Human 1gG1 CH2 sequence with delta b and e (E268)
COTHER INFORMATION: mutations
US-10-959-318-16
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Pred. No. 4.4e-47;
1; Mismatches 3; Indels
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Pred. No. 2.1e-46;
5; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/10/761,593A
CURRENT FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 09/932812
   SOFTWARE: PatentIn version 3.3 SEQ ID NO 16
                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 96.3%;
Matches 105; Conservative
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Best Local Similarity 94.5%;
Matches 103; Conservative
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ORGANISM: Artificial Sequence
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GenCore version
Copyright (c) 1993 - 2005
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November 17, 2005, 07:11:49; Search time 89.0913 Seconds (without alignments) 473.187 Million cell updates/sec

US-09-674-857-1 Title: Perfect score:

1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKAK 109 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

1206590 Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

Searched:

DB seq length: 0 DB seq length: 110 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_16Dec04:* geneseqp1990s:* geneseqp2000s:* geneseqp1980s:* geneseqp20048:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES		
Result No.	Score	HU	Length	DB		Description	
	581	100.0	109	<u>ا</u> ۳	AAY54996	Aay54996 Mutated C	
7	559.5	96.3	110	ო	AAY54998	Aay54998 Mutated C	
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4	554	95.4	109	ო	AAY54997	Aay54997 Mutated C	
5	542	93.3	109	7	ADD25659	6	
9	542	93.3	110	7	AAR27680	Aar27680 Human imm	
7	542	93.3	110	7	AAR41684	Aar41684 Undefined	
80	542	93.3	110	œ	ADH75385	Adh75385 Human IgG	
σ	541	93.1	105	~	AAY42626	Aay42626 Human IqG	
10	540	92.9	109	~	AAR67438	OKT3 #	
11	540	92.9	110	~	AAR41717	Aar41717 Undefined	
12	537	92.4	109	Ŋ	AAE28089	Aae28089 Human imm	
13	537	92.4	110	œ	ADH75415	Adh75415 CH2 regio	
14	536	92.3	110	ω	ADL90103	Ad190103 Human imm	
15	535	92.1	110	œ	ADH75413		
16	534	91.9	109	7	ADD25761	Add25761 Binding d	
17	528	90.9	102	ω	ADJ52129	σ.	
18	526	90.5	102	ω	ADJ52132	Adj52132 CH1 delet	
19	518	89.5	110	7	AAR41713	<u></u>	
20	408	70.2	110	~	AAW71023	Aaw71023 Mus muscu	
21	382	65.7	110	ч	AAP83207	Aap83207 Sequence	
22	344	59.5	72	æ	ADL15711	Adl15711 Human imm	
23	329	56.6		~	AAR75349	Aar75349 C-gamma-1	
24	329	9.95	99	7	AAR75351	Aar75351 C-gamma-1	
25	305	52.5	9/	œ	ADL15713		

Aap83205 Sequence Aap83201 Sequence Aap83201 Sequence Aap83203 Sequence Aap83206 Sequence Adr59138 Human IgG Adr59142 Rhesus mo Adr59141 Rhesus mo Adr59141 Rhesus mo Adr59141 Rhesus mo Adr59141 Crab-eati Aar33314 Variant I Adr59141 Crab-eati	
AAP83205 AAP83201 AAP83201 AAP83202 AAP83203 AAF832306 AAF89138 ADRS9143 ADRS9143 ADRS9141 ADRS9141 AAR33316	AAB53640 ADR59148 ADR59145 AAR33693 ADR59147
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ALIGNMENTS

Binding molecule, CH2 sequence, complement dependent lysis, FegammaRIIb, cell-mediated destruction, human, immunoglobulin G; IgG heavy chain, B cell activation, mast cell degranulation; phagocytosis, vasculitis, Crohn's disease; graft-va-host disease; organ transplant rejection; bone-marrow transplant rejection, autoimmune disease; asthma; allergy; alloimmune thrombocytopaenia, authritis; erythroblastosis foetalis; neconatal alloimmune thrombocytopaenia, goodpastures disease; therapy; sickle cell anaemia; coronary artery occlusion. AAY54996 standard; protein; 109 AA Mutated CH2 sequence Gldeltaab. (first entry) 17-FEB-2000 AAY54996; AAY54996

Synthetic.

WO9958572-A1.

18-NOV-1999

07-MAY-1999;

98GB-00009951. 08-MAY-1998; (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

Williamson LM; Armour KL, Clark MR,

WPI; 2000-039075/03.

Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties.

Claim 12; Fig 17; 81pp; English.

This sequence represents the mutated CH2 molecule Gldeltaab, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant

Claim 12; Fig 17; 81pp; English.

properties.

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domain of a human immunoglobulin G (IgG) heavy chain. The binding molecule is used to bind a target molecule (especially FegammaRIIb causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding molecule is useful for the treatment of graft-vs-molecule. The binding molecule is useful for the treatment of graft-vs-molecule. The binding molecule is useful for the treatment of graft-vs-molecule. The binding molecule is useful for the treatment of graft-vs-cost disease, organ transplant rejection, bone-marrow transplant rejection, autoimmune hacmolytic anaemia, rejection, autoimmune thrombocytopaenia and arthritis), alloimmunity (e.g. chronic or acute inflammatory diseases (e.g. Crohn's, HD) coronary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FegammaR and desirable IgG properties have been retained. The polypeptides do not contain nonhuman amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent for the being able to cross the human placenta through interaction with FCRn for a properties and the forman and placenta through interaction with FCRn for a properties for the forman and placenta through interaction with FCRn forman and placents through interaction with FCRn format and forman and form
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Matches 109; Conservative
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AAY54998
AC AAY5
XX
AX
DT 17-F
DY 17-F
DY 17-F
DY BING
KW BING
KW BOON
KW BOO
                   $$$$$$$$$$$$$$$$$$$$$$$$$$$$
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1; Gaps

Length 110; Indels

96.3%; Score 559.5; DB 3; 98.2%; Pred. No. 1.2e-49; ive 0; Mismatches 1;

Matches 108; Conservative

Query Match Best Local Similarity Sequence 110 AA;

neonatal Fc receptor)

This sequence represents the mutated CH2 molecule Gldeltaac, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without tringgering complement capable of binding a target molecule without tringgering complement capable of binding domain capable of binding a target molecule; and comprises: (a) a binding domain capable of binding a target molecule; and comparing inhibition of a human immunoglobulin G (IgG) heavy chain. The binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule is useful for the treatment of graft-vs. Compresses. The binding molecule, e.g. an antibody, to the target condecule. The binding molecule is useful for the treatment of graft-vs. Complement thrombocytopaenia and arthritis, autoimmune haromolytic anaemia, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia, correction, autoimmunity (e.g. vasculitis), alloimmunity (e.g. chronic or acute inflammanch thrombocytopaenia, asthma and allergy), chronic or acute inflammanch thrombocytopaenia, asthma and allergy), chronic or acute inflammanch thrombocytopaenia, asthma and allergy), chronic or acute inflammanch with gomelecules do not activate complement or trigger cytotoxic activities through FogammaR and desirable complement or trigger cytotoxic activities through FogammaR and desirable immunoganicity. Further, they still bind Porcein A, which is consistent immunoganicity Further, they still bind Porcein A, which is consistent immunoganicity. Further, they still bind Porcein A, which is consistent immunoganicity.

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59
                                                                                                                                                                                                                                                                                                         Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaccutical; gamma-3; gamma-4; diagnostic; agent; tumour; AlDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                 1 APPVAGGPSVFLFPPKFKDTLMISRTPBVTCVVVDVSHEDPBVKFNWYVDGVEVHNAKTK 60
1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                            61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                             60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                               Undefined ORF2 encoded by plasmid pAH4625.
                                                                                                                                                                       AAR41709 standard; protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-US010206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-00800458.
                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9310819-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-NOV-1991;
                                                                                                                                                                                                                                  25-MAR-2003
20-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUN-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                    AAR41709;
                                                                                                                                     RESULT 3
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Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin

(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

99WO-GB001441 98GB-00009951

07-MAY-1999;

18-NOV-1999.

08-MAY-1998;

WO9958572-A1

Williamson LM;

Clark MR,

Armour KL,

WPI; 2000-039075/03.

(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

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                                                                                                                                                                   The sequences given in AAR41707-09 are encoded by the expression vector pAH4625. This vector represents the cloning of the human gamma isotype, gamma-2, with the variable region of the murine monoclonal antibody is 128.1. This plasmid encodes a chimeric monoclonal antibody in which the eavy chain (VH) is derived from a murine source and the sequences encoding CHI. CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ41845), was transfected into SP2/0 cells and clones were isolated. It is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent or diagnostic agent. The conjugate may be used to treat or prevent conversing and Alzhainers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding molecule; CH2 sequence; complement dependent lysis; FogammaRIID; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-va-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopaemia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopaemia; Goodpastures disease; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                 diagnosis and treatment of cancer, AIDS and neurological disorders.
                                                                                                     conjugates specific for transferrin receptor - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.4%; Score 554; DB 2; Length 109; 93.6%; Pred. No. 4.5e-49; Live 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sickle cell anaemia; coronary artery occlusion
                                                                                                                                              Disclosure, Fig 17J; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY54997 standard; protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutated CH2 sequence G2deltaa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 93.6
nes 102; Conservative
(ALKE-) ALKERMES INC
                                                        WPI; 1993-196742/24.
N-PSDB; AAQ43846.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 109 AA;
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                           Friden PM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY54997;
                                                                                                   Antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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this sequence represents the mutated characteries, and is a capable of binding a target molecule without triggering complement of capable of binding a target molecule without triggering complement of dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and domain of a human immunoglobulin G (igG) heavy chain. The binding constant of a human immunoglobulin G (igG) heavy chain. The binding constant constant constant causing inhibition of B cell activation, mast cell degranulation or causing inhibition of B cell activation, mast cell degranulation or capagocycasis). The binding molecule, e.g. an antibody, to the target collecule. The binding molecule is useful for the treatment of graft-vs-corpusation or actorimmunity (e.g. autoimmunity (e.g. vascultis, autoimmune haemolytic anaemia, catoimmune thrombocytopaenia and arthritis), alloimmune his corpusation, autoimmunoty diseases (e.g. Crohn's, HDN chorata alloimmune thrombocytopaenia, asthma and allergy), chronic or acute inflammunoty diseases (e.g. Crohn's, HDN corpusation). The binding molecules do not activate complement or trigger cytotoxic activities do not activate complement or trigger cytotoxic activities through for contain nondimunogenicity. Further they still bind Protein A, which is consistent contain mino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent contain being able to cross the human placenta through interaction with Forn contains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidabetic; antithyroid; mueuroprotective, hinge region; immunoglobulin heavy chain; CH2 constant region; fall constant region; IGG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent call-mediated cytotoxicity; ADCC; complement fixation; antignin; BCG1; myasthenia gravis; Grave's disease; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                              Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding domain-immunoglobulin fusion protein-associated protein #107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                             represents the mutated CH2 molecule G2deltaa, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.4%; Score 554; DB 3; Length 109; 94.5%; Pred. No. 4.5e-49; live 4; Mismatches 2; Indels
Williamson LM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD25659 standard; protein; 109 AA.
                                                                                                                                                                                                                                                                                            Claim 12; Fig 17; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.4
Best Local Similarity 94.5
Matches 103; Conservative
Clark MR,
                                                                     WPI; 2000-039075/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 109 AA;
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64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109

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WPI; 2003-801317/75.
 US2003118592-A1
                                                             Sequence 109 AA;
  26-JUN-2003
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4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE Score 542; DB 7; Length 109; Pred. No. 7.8e-48; 3; Indels 2; Mismatches 93.3%; 95.3%; Matches 101; Conservative Local Similarity Query Match

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Undefined ORF2 encoded by pAH4602.

63

à g g ò 셤 The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide, an immunoglobulin heavy chain can comprising a binding domain polypeptide, an immunoglobulin heavy chain can constant region polypeptide, an immunoglobulin heavy chain can constant region polypeptide, and an immunoglobulin heavy chain can constant region polypeptide. The can constant region polypeptide comprises: a wild-type human Igdi immunoglobulin hinge region polypeptide, a mutated human Igdi immunoglobulin hinge region polypeptide, a mutated human Igdi immunoglobulin hinge region polypeptide, a mutated human Igdi immunoglobulin hinge region polypeptide derived from (a) having 3 or more cysteine residues, where the first cysteine residues, contains 2 cysteine residues, where the first cysteine residues, contains 10 cysteine residues, manual contains no more than one cysteine residues, manual immunoglobulin hinge region polypeptide contains no more than one cysteine residue, and a mutated human Igdi immunoglobulin hinge region polypeptide contains no cysteine residues, and a mutated human Igdi munoglobulin hinge region polypeptide contains no cysteine residues and a mutated human Igdi munoglobulin hinge region polypeptide contains conception and the polympoptide is capable of at least one immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein of construct comprising the polymological activity comprising the binding domain-immunoglobulin fusion protein, a recombinant expression construct composition comprising the binding domain-immunoglobulin fusion protein a resound a carrier, and a carrier, and note of having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, cubject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid are for this parent fusion protein or a B-cell disorder, e.g. melanoma, New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease. immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at sequence.htmlDocID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified. Thompson PA; Disclosure; SEQ ID NO 220; 157pp; English. Ledbetter JA, Hayden-Ledbetter MS, 17-JAN-2001; 2001US-0367358P. 17-JAN-2002; 2002US-00053530. 03-JUN-2002; 2002US-0385691P. 25-JUL-2002; 2002US-00207655 (GENE-) GENECRAFT INC

In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17. The inventor's propose eliminating these allotypes by amino acid changes to agree with the sequences of IgG2, IgG3 and IgG4. None of the allotype sites (1, 2 and 17) are located within the CH2 domain. New "isoallotypes" should be suitable for therapeutic use in all patients. See AAR27678-R27681. (Updated on 25-MAR-2003 to correct PN field.) Humanised antibodies having modified allotypic determinant - useful for matching allotypes in therapy with decreased likelihood of causing undesirable immune responses. 4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE Isoallotype; IgG1 Glm(1,2,17); anti-allotype response; humanised Ab. ; 0 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110 Length 110; 3; Indels 93.3%; Score 542; DB 2; 95.3%; Pred. No. 7.9e-48; ive 2; Mismatches 3; Human immunoglobulin IgG1 CH2 region. AAR27680 standard; protein; 110 AA AAR41684 standard; protein; 110 AA Disclosure; Fig 4c; 57pp; English. 92WO-GB000445. 91GB-00005245 (first entry) (first entry) Matches 101; Conservative (revised) (revised) (LYNX-) LYNXVALE LTD WPI; 1992-349162/42. Local Similarity Sequence 110 AA; 12-MAR-1992; 2-MAR-1991; Homo sapiens. WO9216562-A1 25-MAR-2003 10-MAR-1993 25-MAR-2003 20-OCT-1993 AAR27680; Clark MR; AAR41684; Query Match 65 RESULT 6 AAR27680 RESULT 7 AAR41684 BXHHXXX ö 63 Gaps

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Gaps

63 64

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diseases.
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                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAR41682-85 are encoded by the expression vector, pAH4602. This vector contains open reading frames encoding the heavy chain variable region (VH) of the antibody 128-1, an ampidillin resistance gene and a histidine (histidino) selection marker.

Transcription of the VH gene is from the VH promoter of the murine 27.44 gene. The vector also includes a heavy chain immunoglobulin enhancer and the human gammal constant region (CHI). The VH region of 128.1 was classified by polymerase chain reaction and cloned into plasmid pAH4274.

This was achieved by digesting the plasmid and the product with EcoRV and Nhel. The VH gene was inserted in-frame with the human gammal CH region CH at the 3' end of the VH-J region by means of a Nhel site. 128.1 is anti-human transferrin receptor antibody which binds to the transferrin receptor con brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuro-pharmaceutical or neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
           Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light; chain; variable; constant; region; anti-human; transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                        Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 542; DB 2;
Pred. No. 7.9e-48;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 11K; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH75385 standard; protein; 110 AA
                                                                                                                                                                92WO-US010206
                                                                                                                                                                                        91US-00800458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.3%;
95.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human IgG1 CH2 region.
                                                                                                                                                                                                                  (ALKE-) ALKERMES INC
                                                                                                                                                                                                                                                                    WPI; 1993-196742/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                 N-PSDB; AAQ43844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 110 AA;
                                                                                                             W09310819-A1
                                                                                                                                                                                        26-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-2004
                                                                                                                                      10-JUN-1993
                                                                                                                                                                                                                                           Friden PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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ID ADH7
XX
AC ADH7
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DT 22-,
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The invention relates to a new composition comprises a variant of a parent polypeptide having at least a portion of a Fc region. The variant mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells more effectively than the parent polypeptide and comprises at least one amino acid modification at position 280 in the autoimmune diseases. The present sequence represents e.g., sequence of a human immunoglobulin G, 1gG, CH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising a variant of a parent polypeptide having least a portion of a Fe region, useful in treating e.g., autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;
receptor-binding; binding determinant sequence; anti-IgE antibody;
allergic disease.
Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC; autoimmune disease; human; IgG; immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.3%; Score 542; DB 8; 95.3%; Pred. No. 7.9e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 23; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human IgGl Fcgammal-Fcgamma2 residues.
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                                                                                                                                                                                                                                                                                  20-FEB-2003; 2003US-00370749.
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                                                                                                                                                                                                                                                                                                                                             20-FEB-2002; 2002US-0358161P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watkins JD, Allan B;
                                                                                                                                                                                                                                                                                                                                                                                                            (WATK/) WATKINS J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-070755/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (ALLA/) ALLAN B.
                                                                                                                                                        JS2004002587-A1
                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ното варіеня
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-1991;
                                                                                                                                                                                                                   01-JAN-2004
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(revised)
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                                                                                                                            The anti-human CD3
cell activating and
                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                             Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ43848
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20-OCT-1993
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Matches 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR41717;
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                      field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                        The invention provides immunoglobulin E (IgE) antagonists comprising one or more of the FcepsilonRI receptor-binding determinant sites of human IgE. The antagonists include IgE variants comprising an immunoglobulin template and binding determinant sequences (Dds) CDDds, EFbds and the sequence shown in AAY42581. The CDbds (CD loop binding determinant sequences are selected from the sequences shown in AAY42567-Y4257 and the EFbds (EF loop binding determinant sequences shown in AAY42578-Y4280. The variants are useful in raising and screening anti-IgE antibodies, in the isolation and purification of FerensilonRI receptor and in the treatment and prophylaxis of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                              Immunoglobulin E variants as peptide antagonists useful for raising and screening anti-immunoglobulin E (IGE) antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OKT3; monoclonal antibody; antibody engineering; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.1%; Score 541; DB 2; Length 105; 97.1%; Pred. No. 9.4e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                   Claim 7; Col 63-64; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monoclonal antibody fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR67438 standard; protein; 109
94US-00178583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-US006198
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(first entry)
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Matches 101; Conservative
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                                                                                Jardieu PM, Presta LG;
                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ARCH-) ARCH DEV CORP.
                                                                                                                       WPI; 1999-579941/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 105 AA;
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07-JAN-1994;
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                                                                                                                                                                                                                                diseases
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OKT3

RESULT 10 AAR67438

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                                                                                                                                                     cell activating and immunosuppressive activity, and is used to treat transplant patients to prevent rejection. The antibody can be engineered to contain a human Fc region. By transferring the binding specificity into a human framework, the immunosalicity is reduced without affecting the immunosuppressive activity. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AlDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
New humanised OKT3 antibody with mutated Fc receptor binding region -useful as immunosuppressant to reduce transplant rejection, lacks the T-cell activating side effects of wild type antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAR41715-18 are encoded by the expression vector ppAR4808. This vector represents the cloning of the human gamma isotype, gamma-4, with the variable region of the murine monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody in which the
                                                                                                                                       mouse monoclonal antibody OKT3 (IgG2a) has potent T-
                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                        Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                        92.9%; Score 540; DB 2; L. Llarity 95.3%; Pred. No. 1.3e-47; Conservative 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Undefined ORF2 encoded by plasmid pAH4808.
                                                                                           Page 82-87; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 19J; 151pp; English.
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treatment of various systemic infections. The present sequence is human immunoglobulin G1 (1gG1) Fc region second constant (CH2) domain
                                                                                                          Query Match
Best Local Similarity
Matches 100; Conserv
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                                                                     Sequence 109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH75415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases.
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Matches
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heavy chain (VH) is derived from a murine source and the sequences encoding CHL, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ43845), was transfected into Sp2/0 cells and clones were isolated. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent meurological disorders egg. brain tumours, AIDS, stroke, spilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a modified immunoglobulin (IgG1) which comprises an IgG constant domain having at least one amino acid modification. The immunoglobulins are used in the treatment or prevention of a disease or disorder by passive immunotherapy for vaccinating a subject and for in vivo diagnosis of a subject. The disease and disorders include a gamma globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versushost, lymphoid malignancies and passive immunotherapies and also for the
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                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia; vaccination; hypogammaglobulinaemia; autoimmuno disease; antibacterial; immunosuppressive; lymphoid malignancy; respiratory syncytial virus; anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified immunoglobuling useful in the treatment of autoimmune diseases, comprises at least one amino acid modification relative to a wild-type immunoglobulin constant domain.
                                                                                                                                                                                                                                                                                                                                                                                                       5 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunoglobulin G1 (1gG1) Fc region second constant (CH2) domain.
                                                                                                                                                                                                                                                                                                                                                                                4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                             92.9%; Score 540; DB 2;
95.3%; Pred. No. 1.3e-47;
ive 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 138; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ward ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE28089 standard; protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-2000; 2000US-0254884P. 09-MAY-2001; 2001US-0289760P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-2001; 2001WO-US048432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dall'acqua W, Johnson LS,
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                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                         Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200260919-A2
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AAE28089 RESULT

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                                                                                                              63
                                                                                                                                                                    64
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                                                                                                                                             . LGGGPSVFLFPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                              4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases. The present sequence represents a CH2 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC; autoimmune disease.
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     Length 109
                                                                                                                                                                                                                                                         QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 109
                                                                                                                                                                                                                          64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 108
                                                        3; Indels
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Score 537; DB 5;
Pred. No. 2.5e-47;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cch 92.4%; Score 537; DB 8; al Similarity 94.3%; Pred. No. 2.6e-47; 100; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 53; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  ADH75415 standard; protein; 110 AA
     92.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-2003; 2003US-00370749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-2002; 2002US-0358161P
                               95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-2004 (first entry)
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CH2 region K290S variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Allan B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-070755/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WATK/) WATKINS J D. (ALLA/) ALLAN B.
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parent polypeptide having at least a portion of a Fc region. The variant mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells more effectively than the parent polypeptide and comprises at least one amino acid modification at position 280 in the Fc region. The composition is useful in treating diseases e.g., autoimmune diseases. The present sequence represents a CH2 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising a variant of a parent polypeptide having at least a portion of a Fe region, useful in treating e.g., autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a new composition comprises a variant of a
                                                                                  Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 51; 62pp; English
                                                                                                                                                                                                                                                                                                                                20-FEB-2003; 2003US-00370749
                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2002; 2002US-0358161P
                            CH2 region D280H variant
                                                                                                                                                                                                                                                                                                                                                                                                                                         (WATK/) WATKINS J D. (ALLA/) ALLAN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-070755/07
                                                                                                                                                                                                                    US2004002587-A1
                                                                                                                                                                 Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for generating an immune response to an antigen in a patient. The method comprises administering to the patient an immunoglobulin (Ig) or its portion where the Ig has at least one peptide epitope of the antigen attached to the Ig or its portion and administering the immunoglobulin or its portion in conjunction with a RNA segment. A recombinant human Ig molecule capable of binding to an RC gamma receptor (RogammaR) of an antigen presenting cell (APC) was used to illustrate the invention. The recombinant human Ig molecule comprises a CH3 region (ADL90102), a CH2 region (ADL90103), a hinge region (ADL90104) and a flanking peptide (ADL90105).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generating an immune response to an antigen, useful for generating desired T cell responses comprises administering an immunoglobulin one peptide epitope of the antigen attached to the immunoglobulin.
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                               Score 536; DB 8; Length 110;
Pred. No. 3.3e-47;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Immune response; immunoglobulin; Ig; CH2 region; human.
                                                                                                                                                                                                                                                                                                                                                       SEQ ID 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 11; 154pp; English.
                                                                                                                                                                                        ADL90103 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                    Human immunoglobulin CH2 region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.3%;
94.3%;
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14-MAR-2003; 2003WO-US007995.
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Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASTR-) ASTRAL INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004027049-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                 17-JUN-2004
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                                                                                                                                                                                                                                           ADL90103;
64
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Allan B;

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                                                                                                                            4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                 5 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVHGVEVHNAKTKPREE
                                                                                 Gaps
                                                                                 ö
                                                                                                                                                                                                           QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                       Length 110;
                                                                                 Indels
                                       Query Match 92.1%; Score 535; DB 8; L. Best Local Similarity 94.3%; Pred. No. 4.1e-47; Matches 100; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                   Search completed: November 17, 2005, 07:46:59 Job time : 91.0913 secs
Sequence 110 AA;
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Gaps

; 0

63 64

4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE

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ò g ADH75413 standard; protein; 110 AA.

RESULT 15 ADH75413

(first entry)

22-APR-2004

ADH75413;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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protein search, using sw model OM protein - November 17, 2005, 07:37:49 ; Search time 16.4247 Seconds Run on:

(without alignments) 638.529 Million cell updates/sec

US-09-674-857-1

Perfect score: Sequence:

1 APPVAGPSVFLFPPKFKDTL......CKVSNKGLPSSIEKTISKAK 109

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues

Searched:

44790

Minimum DB seq length: 0 Maximum DB seq length: 110

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* PIR 79:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ige chain C3 regio
Ig kappa chain C r
Ig kappa chain C r
Ig lambda chain C r
Ig lambda chain C r
Ig lambda -1 chain
Ig lambda -2 chain
Ig lambda -2 chain
Ig lambda chain C r
Ig kappa -1 chain C r
Ig lambda chain C r lg gamma-2b chain Description K3HU 168730 168730 168730 198730 198730 198730 101MS 1 8 Query Match Length 133.5 132 131.5 130 127.5 127.5 118.5 118.5 118.5 116.5 115.5 113.5 113.5 112.5 110 110 110 Result

Ig kappa-2 chain Ig kappa-84 chain Ig lambda-3 chain	Ig lambda-2 chain Ig kappa chain C r Ig kappa-B9 chain Ig kappa-B5 chain	Ig gamma-1 chain C Ig light chain C r Ig lambda-2 like ch Ig lambda-2 chain	Ig lambda-2 chain Ig light chain C r Ig lambda chain, C IgE chain C2 regio Ig gamma-3 chain C
K4RBBS G20907 L3MS	S22762 K1RTA K9RB K5RB	S26652 C34509 I57802 L2MS	S22759 D34509 PL0186 I68725 A24629
424	8444	7777	00000
106 106 104	105 106 104	97 78 82 104	105 78 67 107 90
17.0 17.0 16.2	16.2 16.2 15.8	14.6 13.8 13.8	13.8 13.7 11.1 11.0
0 0 0 0 0 4	0 0 0 0 4 4 6 0	83.5 80 80	80 79.5 76.5 64.5 64
30 31 32		37 38 39 40	4 4 4 4 4 1

ALIGNMENTS

of Ig H chain g C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: A30503
R;Gilmore, Gil.; Bardi J.A.; Birshtein, B.K.
J Immunol. 141, 1754-1761, 1988
A;Title: DNA rearrangements affecting both variable and constant regions of A;Reference number: A30503; MUID:88315788; PMID:2842402

A; Molecule type: mRNA A; Residues: 1-88 <GIL>

A;Accession: A30503

A;Cross-references: GB:M21925
A;Experimental source: myeloma cell line MPC11
A;Note: the authors translated the codon GAG for residue 41 as C;Genetics:

C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin F;l-70/Domain: immunoglobulin homology <IMM> A; Introns: 46/3

0; Gaps 47.5%; Score 276; DB 2; Length 88; 63.2%; Pred. No. 2.1e-20; 14; Indels Query Match
47.5%; Score 276; DB
Best Local Similarity 63.2%; Pred. No. 2.1e
Matches 48; Conservative 14; Mismatches

1 SLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDW 60 23 SRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSIYRVVSVLIVLHQDW 82 ð g

83 LNGKEYKCKVSNKGLP ò 셤

ign chain C3 region - mouse (fragment)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cipate: O2-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
CiAccession: 168726
Rishinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-22, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid s
A;Reference number: 154443; MUID:88152907; PMID:3346043

A,Accession: I68726 A,Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-107 «RES» A;Cross-references: GB:M22330; NID:g194455; PIDN:AAA37911.1; PID:g194460 C;Superfamily: immunoglobulin C region; immunoglobulin homology F;22-90/Domain: immunoglobulin homology <IMM>

146731 327390 KIRTB KSRBV

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Risteiner, V.; Chang, J.Y.
FRBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances they
A;Reference number: S02572; MUID:88005152; PMID:3115831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Gene: GDB:IGKC
A/Cross-references: GDB:120088; OMIM:147200
A/Gene: GDB:IGNC
A/Cross-references: GDB:120088; OMIM:147200
A/Gene: GDB:IGN: SDI2-2D12
C/Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kapping laulfide bonds; in some cases, such as IgA and IgM, the subunits associate into law C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/19-88/Domain: immunoglobulin homology < IMM>
A; Accession: A92047
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-13, 'N, 15-106 < TIT>
A; Residues: 1-13, 'N, 15-106 < TIT>
A; Rohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.
Science 169, 16-59, 1970
A; Title: Marcaglobulin structure: variable sequence of light and heavy chains.
A; Reference number: A94242; MUID: 72201507; PMID: 5447531
A; Contents: Waldenstrom's macroglobulin Ou
                                                                                                                                                                                                                                                                                                                                                                                                                                 H.A.; Nevo, S.; Cavalli-Sforza,
                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Molecule type: protein
B; Residues: 1-13, N', 15-16 < KOH>
B; Kutch, J, H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sfo Am. J. Hum. Genet. 48, 613-620, 1991
A; Title: Km typing with PCR: application to population screening. A; Reference number: A37927; MUID:91150772; PMID:1900145
A; Accession: B37927
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A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Malecule type: DNA
A, Residues: 8-106 < KUR>
A, Note: allotype Inv (3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-107 < RES >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Contents: annotation C; Genetics:
                                                                                                                                                                                                                                                                                                                  A;Accession: A94242
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A/Residues: 1-106 <GGT>
A/Rote: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val
B/Gall, W.E.; Edelman, G.M.
A/Reference number: A90565; MuID:71064027; PMID:4923144
A/Contents: annotation; Eu, disulfide bonds
B/Suter, L.; Barnikal, H.U.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
A/Feterence number: A91651; MuID:72188439; PMID:5027703
A/Feterence number: A91651; MuID:72188439; PMID:5027703
A/Residues: 1-106 <SUT>
A/Residues: 1-106 <SUT>
B/Residues: 1-106 <SUT>
A/Residues: 1-106 <SUT>
B/Hitter: A91651
A/Residues: 1-106 <SUT>
B/Hitter: A91651
A/Residues: 1-106 <SUT>
A/Residues: 1-106 <SUT>
B/Hitter: Cloned human and mouse kappa immunoglobulin constant and J region genes conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain C region - human (5) Species: Homo sapiens (man) (2) Species: Homo sapiens (man) (2) Species: Homo sapiens (man) (2) Species: 31-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004 (2) Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02 R;Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M. Biochemistry 9, 3155-3161, 1970 (A) Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequence A;Reference number: A90562; MUID:71064023; PMID:5489770 (A) Contents: myeloma protein Eu
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A;Molecule type: DNA
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rose-references GB:U00241; NID:g33140; PIDN:CAA23823.1; PID:g1335148
A;Note: the sequence was determined from the germline gene
A;Note: the sequence was determined from the germline gene
A;Note: the sequence was determined from the germline gene
A;Note: the sequence was determined from the germline gene
A;Note: the sequence was determined from the germline gene
A;Note: the sequence was determined from the germline gene
A;Reference number: A94417
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A,Residues: 1-56,'Q',58-106 <HI2>
R,Titani, K.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 244, 3550-3560, 1969
A,Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete A;Reference number: A92047; MUID:69234734; PMID:4893682
A;Contents: Bence Jones protein Ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
A;Title: Die volstaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ)
A;Reference number: A91639; MUID:68242259; PMID:5586923
A;Contents: Bence Jones protein Cum
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A;Molecule type: protein
A;Rosidues: 1-44, A',46-56, Q',58-82, L',84-106 <HIL>
A;Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu R;Hilschmann, N.
                                                                                                                                                                                                                                              GVITYLIPPSPLD-LYQNGAPKLTCLVVDLESE-KNVNVTWNQEKKTPVSASOWYTKHHH
                                                                                                                                                                                               GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                           ..
..
                                               Length 107;
                                                                                                                                                                                                                                                                                                                                                                                          NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK 107
                                       ; Score 141; DB 2;
; Pred. No. 5.9e-07;
21; Mismatches 47;
                                           24.3%;
                                   Query Match
Best Local Similarity 31.44
Matches 32; Conservative
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C;Accession: I68730
R;Shinkai, Y:; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid se A;Reference number: I54443; MUID:88152907; PMID:3346043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IgE chain C3 region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                   4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV--EVHNAKTKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDV-SHEDPEVKFN------WYVDGVEV
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM>
F_126-86/Disulfide bonds: #status experimental <math>F_1106/Disulfide bonds: interchain (to heavy chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                     62 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                   cuery match 23.9%; Score 139; DB 1; Length 106; Best Local Similarity 31.5%; Pred. No. 9.2e-07; Matches 34; Conservative 24; Mismarches 11. T-3.
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Ig upsilon chain - duck (fragment)
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Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-105 <SAK>
                                                                                                                 C; Accession: B26167
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                                                                                                                                                                                                                                                                                                                                          Targets chain C region - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Superfamily: Immunoglobulin
C;Superfamily: Immunoglobulin
C;Superfamily: Immunoglobulin
C;Species: Pan troglobulin
C;Species: Pan troglodytes
C;Superfamily: Immunoglobulin
C;Species: Pan troglobulin
C;Species: Pan troglo
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1g lambda chain C region - sheep (fragment)

C;Species Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000

C;Accession: B30554

B;Foley, K.C.; Beh, K.J.

J:Immunol. 142, 708-711, 1989

A;Title: Isolation and sequence of sheep Ig H and L chain CDNA.

A;Reference number: A30554; MUID:89093962; PMID:2492052

A;Accession: B30554

A;Accession: B30554

A;Residues: 1-105 «FOL.

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: hereroterramer; immunoglobulin

F;20-88/Domain: immunoglobulin homology «IMA»
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4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV--EVHNAKTKPR 61
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                                                                                                              54 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK 107
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33.3%; Pred. No. 2.7e-06;
iive 20; Mismatches 42;
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Matches 34; Conservative
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RESULT B26167

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RiParvari, R.; Ziv, E.; Lentner, F.; Tel-Or, S.; Burstein, Y.; Schechter, I.
EMBO J. 6, 97-102, 1987
Aftile: Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germl
A;Reference number: A26167; MUID:87218480; PMID:3107981
A;Accession: B26167
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R.Sakaguchi, N.; Melchers, F.
R.Sakaguchi, N.; Melchers, F.
Atture 324, 579-582, 1986
A.Title: Lambda-5, a new light-chain-related locus selectively expressed in pre-B lympho. A.Reference number: A26434; MUID:87065143; PMID:3024017
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R;Magor, K.B.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
Submitted to the EMBL Data Library, March 1994
A;Description: Evidence from duck immunoglobulin genes that IgY is the common ancestor o
A;Reference number: S43145
A;Accession: S43147
A;Status: preliminary
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Ig lambda chain C region - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig lambda-5 chain C region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1988 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
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C.Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
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A;Arote: the authors translated the codon TAC for residue 84 as Thr
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKQTNNKYMVSSYLTLISDQWMPHSRYSCRVTHEG--NTVEKSVSPAE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 103;
                                                                                                                                                                                                                                                                                                                                                                       A;COSB-references: UNIPROT:P20763; GB:M33049
A;Note: 90-Asp was found in one cDNA clone
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heteroteramer; immunoglobulin
F;21-87/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
22.7%; Score 132; DB 2;
Best Local Similarity 29.9%; Pred. No. 4.4e-06;
Matches 32; Conservative 25; Mismatches 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.4%; Pred. No. 5e-06; ive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.6%; Score 131.5;
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Cipate: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
Cipate: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
Cipacession: $2276
Cipacession: 
                                                                    2 PKSSPSVTLFPPSSEEL----ETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus spretus (western wild mouse)
C;Date: 31-Dec-1988 #sequence_revision 07-Sep-1990 #text_change 21-Jan-2000
C;Datession: 800259
EMBO J. 7, 117-122, 1988
A;Title: Conservation of the immunoglobulin C-lambda-5 gene in the Mus genus.
A;Reference number: 800259; MUID:88196070; PMID:3129289
         PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 106;
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                                                                                                                                                                                                                                                SB SKQSNNKYMASSYLTLTARAWERHSSYSCQVTHEG--HTVEKSLSRA 102
                                                                                                                                                                                               62 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: not compared with conceptual translation A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-106 < MANA A; Note: the sequence was translated from the germline gene C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;21-89/Domain: immunoglobulin homology < IMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Best Local Similarity 30.8%; Pred. No. 1.3e-05;
Matches 33; Conservative 19; Mismatches 48
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30.6%; Pred. No. 1.6e-05;
tive 23; Mismatches 45
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C;Species: Mus musculus (house mouse)
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Best Local Similarity 30.69
Matches 33; Conservative
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A,Rocession: A93922
A,Rocession: A93922
A,Rocession: A93922
A,Rosidues: 1-105 < ASEL-A,Cross-references: UNIPROT: P01843; GB:J00587; NID:g197754; PIDN:AAB59672.1; PID:g197761
A,Cross-references: UNIPROT: P01843; GB:J00587; NID:g197754; PIDN:AAB59672.1; PID:g197761
B,Bothwell, A.L.M.; Paskind, M.; Schwartz, R.C.; Sonenshein, G.E.; Gefter, M.L.; Baltimc Nature 290, 65-67, 1981
A,Rocession: A93251; MUD:g1148806; PMID:6259534
A,Rocession: A93251; MUD:g1148806; PMID:6259534
A,Rocession: A93251
A,Rocession: A93282
A,Rocession: A93382
A,Rocession: A,Rocession: A,Rocession: A,Rocession: A,Rocession: A,Rocession: A,Rocession: A,Rocession: A,Rocess
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Rolleus: 1-18, 'TE', 21-55,'E', 57-74,76-80,'SH', 83-85,'S', 86-95,'Q', 97-105 <APP>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGPQSCSPIQIFVVPPSP-GSLYIRQDAKVHCLVVNLP-SDASLSISWTREKSGALRPDP
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A; Residues: 1-105 < BO2>
A; Residues: 1-105 < BO2>
A; Residues: 1-105 < BO2>
A; Note: the sequence was determined from the differentiated gene
B; Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
A; Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
A; Contents: myoloma protein MOPC 104E
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F:27-86/Disulfide bonds: #status predicted
F:104/Disulfide bonds: interchain (to heavy chain) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK 107
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                                                                                                                                                                                                                                            Length 110;
                                                 A,Residues: 1-110 <MAG>
A,Cross-references: EMBL:X78355; NID:g468612; PID:g468613
C,Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                       ch 22.4%; Score 130; DB 2; Length 11 Similarity 28.4%; Pred. No. 7.5e-06; 31; Conservative 22; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig lambda-1 chain C region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1991 #sequence_revision 29-Jun-1991 #text.
C;Accession A93922; A93251; A93282; A93775; A0126
R;Selsing, E.; Miller, J.; Wilson, R.; Storb, U.
Proc. Natl. Acad. Sci. Us.A. 79, 4681-4685, 1982
A;Title: BV-lution of mouse immunoglobulin lambda genes.
A;Reference number: A93922; MUID:83014953; PMID:6812053
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Best Local Similarity 30.8 Matches 33; Conservative
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity
A; Molecule type: DNA
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A;Residues: 1-105 <HIE>
A;Cross-references: GB:J00253; NID:g186118; PIDN:AAA59107.1; PID:g186127
A;Note: six tandem lambda-type genes were identified and the three most 5' were sequence
                                                                                                                                                                                                                                                                                                                                A,Cross-references: GDB:120691; OMIM:147220
A;Map position: 22q11.2-22q11.2
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap. C;Complex: An immunoglobulin heteroteramer subunit consists of two identical light (kap. C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;20-88/Domain: immunoglobulin homology <IMM>F;27-86/Disulfide bonds: #status experimental
F;104/Disulfide bonds: interchain (to heavy chain) #status experimental
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A;Note: the authors translated the codon GTC for residue 84 as Thr and ACC for residue 6. Superfamily: immunoglobulin c region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Hayzer, D.J.; Duvoisin, R.M.; Jaton, J.C.
Biochem. J. 245, 691-697, 1987
A;Title: cDNA clones encoding rabbit immunoglobulin lambda chains. Evidence for length
A;Reference number: A90338; MUID:88024122; PMID:3117050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substitute for human antibodies:
                                                                                                                                              ce (lambda-3)
C;Comment: The sequence shown is the Kern-/Oz-/Mcg- chain found in proteins Sh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH-NAKTKPR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PAVTPSVILFPPSSEE--LKDNKATLVCLIND--FYPGTVKVNWKADGTPVTQGVDTTQP 57
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C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C;Accession: H32529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: S26654
R; Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L. Hun. Antibodies Hybridomas 1, 23-26, 1990
A; Title: Potential of primate monoclonal antibodies to substitute for human A; Reference number: S26652; MUID:91355693; PMID:2129418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig lambda chain C region - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIS 106
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Best Local Similarity 28.6%; Pred. No. 9.7e-
Matches 30; Conservative 23; Mismatches
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Ig lambda chain C region (clone pDH2) - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: H32529
A, Molecule type: mRNA
A, Residues: 1-105 <HAY>
                                                                                                                                                                                                                                                                                            A; Gene: GDB: IGLC2; IGLC
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Best Local (
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A;Contents: Bence-Jones protein Nig-64
A;Accession: A91970
A;Contents: Bence-Jones protein Nig-64
A;Molecule type: protein
A;Residues: 1-105 < KQM>
A;Reference number: A91650; MUID:71150136; PMID:5549568
A;Contents: Bence Jones protein Kern
A;Recession: A91650
A;Molecule type: protein
A;Accession: A91650
A;Molecule type: A91650

                                        Ig lambda chain C regions - human (Species: Homo sapiens (man) (C)Species: Homo sapiens (man) (C)Species: Homo sapiens (man) (C)Species: Homo sapiens (man) (C)Date: 31-Jan-1981 #sequence_revision 31-Jan-1981 #text_change 09-Jul-2004 (C)Accession: A92057; A90243; A91970; A91650; A90375; B90381; A93268; A02125 (C)Accession: A92057; A91970; A91650; A90375; B90381; A93268; A02125 (C)Accession: A545, 2171-2176, 1970 (C)Accession: A545, 2171-2176, 1970 (C)Accession: A545, 2171-2176, 1970 (C)Accession: A571-2176, A771-110: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete A;Reference number: A92057; MUID:70166723; PMID:4909564
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A; Rolecule type: protein
A; Residues: 1-81, K', 83-105 < CHE>
A; Residues: 1-81, K', 83-105 < CHE>
A; Residues: 1-81, K', 83-105 < CHE>
A; Rote: this chain has the Oz+ marker, 82-Lys (instead of Arg)
A; Note: this chain has the Oz+ marker, 82-Lys (instead of Arg)
B; Poljak, R.J.; Amzel, L.M.; Avey, H.E.; Chen, B.L.; Phizackerley, R.P.; Saul, F.
Proc. Natl. Acad. Sci. U.S.A. 71, 3440-3444, 1974
A; Title: The three-dimensional structure of the Pab' fragment of a human myeloma immunog
A; Reference number: A93789; MUID:75046825; PMID:4215080
A; Contents: annotation; Newm; X-ray crystallography, 2.0 angstroms
B; Fett, J.W.; Deutsch, H.F.
A; Title: Primary structure of the Mcg lambda chain.
A; Reference number: A90381; MUID:75013804; PMID:4415202
A; Contents: Bence Jones protein Mcg; partial sequence
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-4,'N',6,'T', 8-44,'G',46-55,'K',57-105 «FET>
A;Note: this sequence has the Kern+ marker, 45-GJy, and the Mcg+ marker, 5-Asn, 7-Thr, a
R;Edmundson, A.B.; Ely, K.R.; Abola, E.E.; Schiffer, M.; Panagiotopoulos, N.
Biochemistry 14, 3953-3961, 1975
A;Title: Rotational allomerism and divergent evolution of domains in immunoglobulin ligh
A;Reference number: A90391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R,Milstein, C.; Clegg, J.B.; Jarvis, J.M.
Biochem. J. 110, 631-652, 1968
A;Title: Immunoglobulin lambda-chains. The complete amino acid sequence of a Bence-Jones
A;Reference number: A90243; MUID:6908380; PMID:4883841
A;Contents: Bence Jones protein X; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: Comparative studies on the structure of the light chains of human immunoglobuli
A,Reference number: A91970; MUID:83186114; PMID:6404900
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A;Reference number: A93268; MUID:82080680; PMID:6273747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kametani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
J. Biochem. 93, 421-429, 1983
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R;Hieter, P.A.; Hollis, G.F.; Korsmeyer, S.J.; Waldmann, T.A.; Leder, P.
Nature 294, 536-540, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: P01842
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A; Accession: A93268

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7; Gaps
                                                                                                                                           Query Match 20.2%; Score 117.5; DB 2; Length 98; Best Local Similarity 30.1%; Pred. No. 0.00011; Matches 31; Conservative 20; Mismatches 45; Indels
A;Accession: S26654
A;Status: translation not shown
A;Molecule type: mRNA
A;Molecule 1-98 «EHR>
A;Residues: 1-98 «EHR>
A;Cross-references: BMEL:X65286
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin homology <IMM>
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Search completed: November 17, 2005, 07:55:07 Job time: 17.4247 secs

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07:13:34 ; Search time 77.1461 Seconds (without alignments) 723.518 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-674-857-1 Title:

Perfect score:

1 APPVAGPSVFLFPPKPKDTL.....CKVSNKGLPSSIEKTISKAK 109 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

301588 Total number of hits satisfying chosen parameters:

length: 0 length: 110 Minimum DB seq Maximum DB seq

Listing first 45 summaries 100% Post-processing: Minimum Match 08 Maximum Match 10

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	4.	<u> </u>	_	enm .	mus	Q8tcj5 homo sapien		P01847 oryctolagus			P20766 rattus norv		P03984 oryctolagus		P01839 oryctolagus	P01835 rattus norv	P01845 mus musculu		_	_	P01844 mus musculu	_			Q7xzf9 oryza sativ	-	Q61bw2 mus musculu	-	P79659 oncorhynchu	P79660 oncorhynchu	O8fbv4 escherichia
SUMMARIES	OI	KAC HUMAN	LAC_CHICK	LACI MOUSE	LACS MUSSP	LACS MOUSE	QBTCJS	LAC HUMAN	LAC RABIT	KAC4 RABIT	LAC PIG	LAC1 RAT	KAC_MOUSE	KAC6_RABIT	LAC2_RAT	KACB_RABIT	KACB_RAT	LAC3 MOUSE	KACA_RAT	KAC9_RABIT	KAC5_RABIT	LAC2_MOUSE	Q99JC1	QBKYIO	Q6EZI5	Q7XZF9	Q6LBV9	Q6LBW2	Q9JKP1	P79659	P79660	Q8FBY4
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di	Ouery Match	m	ď.	۲.	۲.	21.1	ö	0	19.5	σ	α	18.6	18.4	17.9	17.0	17.0	17.0	16.2	16.2	16.0	15.8	13.8	13.8	11.4	11.4	10.8	10.7	10.6	10.5	10.4	10.4	10.3
	Score	139	132	127.5	126.5	122.5	121.5	118.5	113.5	112.5	108.5	108	107	104	66	66	66	94	94	93	92	80	80	99	99	63	62	61.5	61	60.5	60.5	9
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180697 homo sapien Q31248 peromyscus Q31158 mus musculu Q768w8 uncultured Q19471 mus musculu Q99quh8 mus musculu Q99quh8 mus scrofa Q8c5t6 mus musculu Q8c5t6 mus musculu Q31261 rattus norv Q768w5 uncultured P13123 sulfolobus Q26327 trypanosoma	Q971t6 sulfolobus
SNSP_HUMAN Q31248 Q31158 Q31158 Q768W8 Q768W8 Q19471 Q19471 Q9CUH8 Q8HX76 Q31261 Q768W5 Q31261 Q768W5 DN71_SULAC	ALB2_SULTO
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000000000000000000000000000000000000000	9.8
88 88 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	57
W W W W W W W W W W W W W W W W W W W	45

ALIGNMENTS

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MEDLINE=72188439; PubMed=5027703;
Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of kappar-type, subgroup 3 (Bence-Jones protein
Ti). IV. The complete amino acid sequence and its significance for the
mechanism of antibody production.";
Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE (BENCE-JONES PROTEIN ROY).
Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
Steinmetz-Kayne M., Suter L., Watanabe S.;
(In) Franek F., Shugar D. (eds.);
Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
                                                                                                                                                                                                                                           MEDIINE=71064023; PubMed=5489770;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VI. Amino
acid sequence of the light chain.";
Biochemistry 9:3155-3161(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=81042304; PubMed=6775818; DOI=10.1016/0092-8674(80)90168-3;
Hieter P.A., Max E.E., Seldman J.G., Maizel J.V. Jr., Leder P.;
"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";
                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                  Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
22-CCT-2004 (Rel. 45, Last annotation update)
1g kappa chain C region.
                106 AA
                PRT;
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MEDLINE=68242259; PubMed=5586923;
Hilschmann N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE (BENCE-JONES PROTEIN II).
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MEDLINE=71064027; PubMed=4923144;
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SEQUENCE (MYELOMA PROTEIN EU)
                STANDARD;
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Cell 22:197-207(1980)
                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                             NCBI_TaxID=9606;
              KAC HUMAN
P01834;
                                                                                                                      Name=IGKC;
KAC HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Abdominal adipose tissue;
MEDLINE-98849779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
MEDLINE-98849779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
MEXERIDAR K.E., Sletten K., Westermark P.;
"Extended analysis of AL-amyloid protein from abdominal wall subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
Biochem. Biophys. Res. Commun. 245.713.716 (1998).
-!- MISCELLANEOUS: The EU sequence has the INV (3) allotypic marker, Ala-45 and Val-83. The ROY sequence has the INV (1,2) allotypic marker, Ala-45 and Leu-83.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
  complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1. PROSITE; PS50815; IG LIKE; 1. PROSITE; PS508290; IG MHC; 1. 3D-structure; Direct protein sequencing; Immunoglobulin C region;
                                                                                                                                               Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. Complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3560(1969).
                                                                                                                                                                                                                                                                                                                      Kohler H., Shimizu A., Paul C., Putnam P.W.; "Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interchain (with a heavy chain).
V -> L (in INV(1,2) marker).
FTIG=VAR_003897.
D -> N (in Ref. 7 and 8).
E -> Q (in Ref. 5 and 6).
                                                   Joppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
                                                                                                                                                                                                                                                                       SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
MEDLINE=70201507; Pubmed=5447531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO, GO:0003823; F:antigen binding; NAS. GO; GO:006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
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                                                                                                 SEQUENCE (BENCE-JONES PROTEIN AG)
                                                                                                                             MEDLINE=69234734; PubMed=4893682
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PDB: 1D5B; X-ray; A/L=1-103.
PDB: 1D5I; X-ray; L=1-103.
PDB: 1DFZ; X-ray; L=1-103.
PDB: 1HEZ; X-ray; L=1-106.
PDB: 1HKZ; X-ray; L=1-106.
PDB: 1MX, X-ray; L=1-106.
PDB: 1MM; X-ray; L=1-106.
PDB: 1MM; X-ray; L=1-106.
H-InVDB: HXX0021121; --
MIM; 147200; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV--EVHNAKTKPR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=87218480; PubMed=3107981;
Parvar: R., Ziv E., Lentner F., Tel-Or S., Burstein Y., Schechter I.;
"Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germline V lambda genes and allotypes of the C lambda locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 BEOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P01842; 7FAB.
InterPro; IPR007110; 1g-like.
InterPro; IPR003059; 1g_c1.
InterPro; IPR003006; 1g_MHC.
Efam; PF00047; 1g; 1.
SMART; SM00407; 1Gc1; 1.
PROSITE; PS00290; 1G_MHC; 1.
Immunoglobulin C region; Immunoglobulin domain; Polymorphism.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.9%; Score 139; DB 1; Length 106; Best Local Similarity 31.5%; Pred. No. 6.2e-06; Matches 34; Conservative 24; Mismatches 44; Indels
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11609 MW; 51984D1FDD372CE8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-PEB-1991 (Rel. 17, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Ig lambda chain C region.
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103 1
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103 AA;
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106 AA;
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P20763;
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                                                                                                                 3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 62
                                                                                                                                          Appella E.;
"Amino acid sequences of two mouse immunoglobulin lambda chains.";
Proc. Natl. Acad. Sci. U.S.A. 68:590-594 (1971).
-!- MISCELLANBOUS: The MOPC 315 cell line produces 2 light chains, 1
normal lambda-2 chain and 1 abnormal lambda-1 chain that is
missing a large part of the V region. The C region sequence (shown
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=82220143; PubMed=6283385;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baltimore D.; "Somatic variants of murine immunoglobulin lambda light chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=81148806; PubMed=6259534;
Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
Gefter M.L., Baltimore D.;
"Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
Nature 290:65-67(1981)
                                                                      9
                                                                                                                                                                                                            63 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                       ROSNSOYMASSYLSLSASDWSSHETYTCRVTHNG--TSITKTLKRSE 102
                      Length 103;
                                                                 44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=83014953; PubMed=6812053; Selaing E., Miller J., Wilson R., Storb U.; Selaing E., Miller J., Wilson R., Storb Genes."; Evolution of mouse immunoglobulin lambda genes."; Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
               22.7%; Score 132; DB 1;
29.9%; Pred. No. 2.9e-05;
ive 25; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
19 lambda-1 chain C region.
Mus musculus (Mouse)
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MEDLINE-71107854; PubMed=5276767;
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PDB; 1JNH; X-ray; A=1-105.
InterPro; IPR000710; Ig-like.
InterPro; IPR003006; Ig-MHC.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (MOPC 315)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J00582; AAA51636.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (S43).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 298:380-382(1982).
                                                                 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                  LAC1 MOUSE
               Query Match
Best Local
                                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                                                                                                                    LACI MOUSE

ID LACI MOUSE

ID LACI MOUSE

DT 21-JUL-
DE 19 192-JUL-
DE 19 192-JUL-
DE 19 192-JUL-
DE 1
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                                                                 Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : ||| ||| :: | : | | | | PKSSPSVTLFPPSSEEL----ETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88196070; PubMed=3129289;
Mami F., Cazenave P.A., Kindt T.J.;
"Conservation of the immunoglobulin C lambda 5 gene in the Mus gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
3D-structure; Direct_protein sequencing; Immunoglobulin C region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SB SKOSNNKYMASSYLTLTARAWERHSSYSCOVTHEG--HTVEKSLSRA 102
                                                                                                                                          Interchain (with heavy chain).
ET -> TE (in Ref. 4).
Q -> E (in Ref. 4).
Missing (in Ref. 4).
HS -> SH (in Ref. 4).
S -> SS (in Ref. 4).
E -> Q (in Ref. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11575 MW; A89F2B09BCFCA018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBO J. 7:117-122(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.9%; Score 127.5; DB 1
30.8%; Pred. No. 8.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Ig lambda-5 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105
                                                                                                   Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 30.89
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                            Immunoglobulin domain.
NON TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10096;
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DISULFID
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6 1
27
104 1
105 AA;
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DOMAIN
DISULFID
DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TCJ5
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                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                       QRTCJE
    SETE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKSDPLVTLFLPSLKNL----QANKVTLVCLVSEFYPGTLVVDWKVDGVPVTQGVETTQP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87065143; PubMed=3024017;
Sakaguchi N., Melchers F.;
"Lambda 5, a new light-chain-related locus selectively expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pre-B lymphocytes.";
Nature 324:579-582(1986).
-!- TISSUE SPECIFICITY: Selectively expressed in pre-B lymphocytes.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                              21.8%; Score 126.5; DB 1; Length 105; 30.6%; Pred. No. 0.0001; live 23; Mismatches 45; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S SKOTNNKYMVSSYLTLISDOWMPHSRYSCRVTHEG--NTVEKSVSPAE 103
                                                                                                                                                                                                                                                                                                                                104 Interchain (with heavy chain).
11674 MW; AAB417DF68471A17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGT:96529; IGH-5.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR0033006; Ig-MHC.
SWART; SM00407; IGG1; I.
PROSITE; PS50835; IG LIKE; I.
PROSITE; PS00290; IG-MHC; FALSE NEG.
Immunoglobulin C region; Immunoglobulin domain.
NON_TER
                                                                         InterPro; IPR003199; Ig-like.
InterPro; IPR003597; Ig-like.
InterPro; IPR003006; Ig-MHC.
Fram; PF00047; ig. 1.
SWART; SW00407; IG-1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
IRWINOGLODULIN C region; Immunoglobulin G main.
NOW TER 6 100 Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
11 ambda-5 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 AA
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M30387; -; NOT_ANNOTATED_CDS
HSSP; P01843; 1JNH.
                                         EMBL; M35582; AAA39152.1; -.
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.69
Matches 33, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                           104
                                                                                                                                                                                                                                                                                                         27
104
105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                  P01843; 1JNH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LACS MOUSE
ID LACS MOUSE
AC P207\overline{6}4;
                                                                                                                                                                                                                                                                                                         DISULFID
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28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PKSDPLVTLFLPSLKN-LQPTR-PQLVCLVSE--FYPGTLVVDWKVDGVPVTQGVETTQP 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Lymph node;
The German cDNA Consortium;
The German cDNA Consortium;
The German cDNA Consortium;
The German C., Dauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AL713800; CAD28551.1;
THSSP; P01842; ILIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 PKAAPSVTLFPPSSEE--LQANKATLVCLISD--FYPGAVTVAWKADSSPVKAGVETTTP
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp667J0810 (Fragment).
Name=DKFZp667J0810;
Mame=DKFZp667J0810;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 106;
                                                                                                                                                                                                                                                         Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
100 Ig-like.
86
104 Interchain (with heavy chain).
11678 MW; 1F210915904A86AS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 20.9%; Score 121.5; DB 2 Local Similarity 29.5%; Pred. No. 0.00033; Pred 31; Conservative 22; Mismatches 45
                                                                                                                                                                                                                                                    21.1%; Score 122.5; DB 1
31.5%; Pred. No. 0.00026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Name=IGLC1;
                                                                                                                                                                                                                                                                                                                                                    34; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 AA
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   history, 1970, 1971.
InterPro; 1970, 1971.
InterPro; 1970, 1971.
InterPro; 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 1970, 197
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Best Local Similarity
Matches 34; Conserv
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X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
Edmundson A.B., Ely K.R., Abola E.E., Schiffer M., Panagiotopoulos N.;
"Rotational allomerism and divergent evolution of domains in
immunoglobulin light chains.";
                                                                                                                                            The
                                                                                                                                                                                                                            Milstein C., Clegg J.B., Jarvis J.M.; "Immunoglobulin lambda-chains. The complete amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                            Ponstingl H., Hess M., Hilschmann N.;
"Structural rule of antibodies. Primary structure of a monoclonal immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-protein Kern). V. The complete amino acid sequence and its genetic interpretation.";
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human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=74109253; PubMed=4814727;
Chen B.L., Poljak R.J.;
"Amino acid sequence of the (lambda) light chain of a human myeloma
immunoglobulin (IgG New).";
Biochemistry 13:1295-1302(1974).
                                                                                                                                                                                                                                                                                                                                   "Comparative studies on the structure of the light chains of human immunoglobulins. IV. Assignment of a subsubgroup."; J. Biochem. 93:421-429(1983).
                                                                                                                                            protein. 3.
                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=75046825; PubMed=4215080;
Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The three-dimensional structure of the fab' fragment of a human myeloma immunoglobulin at 2.0-A resolution."; Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
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Titani K., Wikler M., Shinoda T., Putnam P.W.;
"The amino acid sequence of a lambda type Bence-Jones protein.
complete amino acid sequence and the location of the disulfide
                                                                                                                                                                                                                                                                                                   MEDLINE-83186114; PubMed-6404900;
Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.
                                                                                                                                                                                                      SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-75013804; PubMed=4415202;
Fett J.W., Deutsch H.F.;
"Primary structure of the Mcg lambda chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
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                                                                                                                                                                                                                                                                                         SEQUENCE (BENCE-JONES PROTEIN NIG-64).
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE (BENCE-JONES PROTEIN KERN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stoppini M., Beliotti V., Negri A., "Characterization of the two unique immunoglobulins.";
                                                                                                                                                                              Biol. Chem. 245:2171-2176(1970).
                                                                                                         SEQUENCE (BENCE-JONES PROTEIN SH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Biochem. 228:886-893(1995)
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=71150336; PubMed=5549568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95255298; PubMed=7737190;
                                                                                                                                                                                                                  MEDLINE=69088380; PubMed=4883841;
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                                                                                                                                                                                                                                                     Bence-Jones protein.";
Biochem. J. 110:631-652(1968).
                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE (DOT)
            Name=IGLC2;
                                    Name=IGLC3;
                                                                                                                                                                                                                                                                                                                            Shimizu A.;
                                                                                                                                                                    bridges.";
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                                                                                                                                                                                                                                                                                                                                                                                                                  -I.—MISCELLANEOUS: The sequence shown is the Kern-/Oz-/Mcg- chain found in proteins SH, X, and NIG-64. The Kern protein has the Kern+ marker, the NEWM protein has the Oz+ marker, the Mcg protein has the Kern+ marker, and the Mcg+ marker.

-I.—MISCELLANEOUS: Six tandem lambda-type genes were identified and the J most S, were sequenced. These correspond to the Mcg sequence (lambda-1), the Kern-/Oz- sequence (lambda-1), and the Kern-/Oz-
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=82080680; PubMed=6273747;
Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
"Clustered arrangement of immunoglobulin lambda constant region genes
                                                                            MEDLINE=90131913; PubMed=2515285;
Bly K.R., Herron J.N., Harker M., Edmundson A.B.;
"Three-dimensional structure of a light chain dimer crystallized in
water. Conformational flexibility of a molecule in two crystal
forms ";
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PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
Drattucture; Bence-Jones protein; Direct protein sequencing; Immunoglobulin C region; Immunoglobulin domain.
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/FTId=VAR 003898.

S -> T (in MCG+ marker).

/FTId=VAR 003899.

S -> G (in Kern+ marker).

/FTId=VAR 003900.

/FTId=VAR 003901.

/FTId=VAR 003901.

/FTId=VAR (in OCF+ marker).
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                                                    K-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF MCG
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EMBL; L38562; AAB36581.1; ALT INIT.
EMBL; X51754; CAB38569.1; ALT_INIT.
EMBL; X51755; CAA36049.1; -.
EMBL; X51755; CAA36051.1; -.
Biochemistry 14:3953-3961(1975).
                                                                                                                                                                                                          J. Mol. Biol. 210:601-615(1989).
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PDB; 1AQK; X-ray; L=1-105.
PDB; 1LIL; X-ray; A/B=1-105.
PDB; 2MCG; X-ray; --
PDB; 7FAB; X-ray; --
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Genew, HGNC:5856; IGLC2.
Genew, HGNC:5857; IGLC3.
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PAVTPSVILEPPSSEE--LKDNKATLVCLISDFYPR--TVKVNWKADGNSVTQGVDTTQP 57
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05-JUL-2004 (Rel. 44, Last annotation update)
15 Jambda chain C region.
Oryccolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Lagomorpha; Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garcia I., Jaton J.-C.;
"The primary structure of the constant region of Basilea-rabbit immunoglobulin lambda-chains.";
Biochem. J. 197:177-133(1981.";
-!- MISCELLANEOUS: This lambda chain expresses the c7 allotypic
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11484 MW; B427513272E8663D CRC64;
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02130; L7RB.
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SKOSITE; PS00290; IG_MHC; PALSE NEG.
Direct protein sequencing; Immunoglobulin C region; Immunoglobulin domain.
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28.6%; Pred. No. 0.00064;
iive 23; Mismatches 45
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01-FEB-1991 (Rel. 17, Last seq
05-JUL-2004 (Rel. 44, Last ann
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InterPro, IPR007110, Ig-like.
InterPro, IPR003597, Ig_cl.
InterPro, IPR003006, Ig_MHC.
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SMART; SM00407; IGC1
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105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=75133568; PubMed=1091650;
Chen K.C.S., Kindt T.J., Krause R.M.;
Chen K.C.S., Kindt T.J., Krause R.M.;
"Primary structure of the L chain from a rabbit homogeneous antibody
to streptococcal carbohydrate. II. Sequence determination of peptides
from tryptic and peptic digests.";
J. Biol. Chem. 250:3289-3296(1975).
-!- MISCELLANBOUS: This chain was obtained from antibody to the
specific carbohydrate of group C Streptococci and was isolated
from the serum of a single rabbit.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-83300036; PubMed-6412231;
MEDLINE-83300036; PubMed-6412231;
Emorine L., Dreher K.L., Kindt T.J., Max B.E.;
"Rabbit immunoglobulin kappa genes: structure of a germline b4 allotype J-C locus and evidence for several b4-related sequences in the rabbit genome.";
Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=82060334; PubMed=6795636;

Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;

"Nucleotide sequence of constant and 3' untranslated regions of a kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";

Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1g kappa-b4 chain C region.
1g kappa-b4 chain C region.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
62 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                     58 SKQSNNKYAASSFLHLTANQWKSYQSVTCQVTHEG--HTVEKSLAPAE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 112.5; DB 1; Length 103; Pred. No. 0.0024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interchain (with a heavy chain)
N -> D (in Ref. 3).
SFC5ACC8B60E68DB CRC64;
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                                                                                                                                                                                                                             103 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01837; 1KCV.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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11043 /
                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95
85
103
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Matches

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.6%; Score 108; DB 1; 25.2%; Pred. No. 0.0068;
                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin C region; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Mismatches
                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                             EMBL; M22520; AAA41419.1; ALT_INIT.
HSSP; P01843; 1JNH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 I)
11565 MW;
                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfan; PP00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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tes 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain
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ID KAC MOUSE
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                              3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE----VHNAKT 58
                                                2 PVA-PTVLIFPPAADQ--VATGTVTIVCV---ANKYFPDVTVTWEVDGTTQTTGIENSKT 55
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   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin lambda chains.";
Biochemistry 16:3765-3772(1977).
-!- MISCELLANEOUS: This chain was obtained from a mixture of normal
                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g lambda-1 chain C region.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 105;
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=78000254; Pubmed-409425;
Novotny J., Franek F., Margolies M.N., Haber E.;
"Amino acid sequence of normal (microheterogeneous) porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 Interchain (with heavy chain) 11003 MW; 3817AAEBD747C396 CRC64;
                                                                                       59 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE 102
 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Indels
                                                                                                            56 P--QNSADCTYNLSSTLTLTSTQYNSHKEYTCKVT-QGTTSVVQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulins.
--- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02129; LIPG.
HSSP; P01042; 2MCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00407; iGc1; 1.
PROSITE; PS0035915; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin C region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 108.5; DB : Pred. No. 0.0061;
                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Ig lambda chain C region.
                                                                                                                                                                                                    105 AA
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19; Mismatches
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                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig_MHC.
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28.4%;
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33; Conservative
                                                                                                                                                                                                  STANDARD;
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104
105 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                             Sus scrofa (Pig)
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P20766;
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SEQUENCE FROM N.A.
MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
Steen M.L., Hellman L., Pettersson U.;
"The immunoglobulin lambda locus in rat consists of two C lambda genes and a single V lambda gene.";
Gene 55:75-84(1987).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE=73053310; PubMed=4638343;

MEDLINE=73053310; PubMed=4638343;

MEDLINE=73053310; PubMed=4638343;

MEDLINE=73053310; PubMed=4638343;

MEDLINE=7305310; PubMed=46383435;

MEDLINE=7305310; PubMed=4638345;

MEDLINE=7305310; PubMed=4638345;

MEDLINE=730531
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MEDLINE-73008889; PubMed=5073237;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
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CBF71811F4BC878A CRC64;
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PubMed=6424123;
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Max E.E., Maizel J.V. Jr., Leder P.;
"The nucleotide sequence of a 5.5-kilobase DNA segment containing the mouse kappa immunoglobulin J and C region genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-81198949; PubMed-6785724;
Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;
"DNA sequence of the constant gene region of the mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88329081; PubMed-3138116; de Waele P., Fiers W.; de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.; "Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline
                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=82059477; PubMed=6170937;
Hamlyn P.H., Gait M.J., Milstein C.;
"Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxynucleotide method of RNA sequencing.";
                           MEDLINE=19084137; PubMed=103625; DOI=10.1016/0092-8674(78)90290-8; Mannlyn P.H., Brownlee G.G., Cheng C.C., Gait M.J., Milstein C.; "Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the dideoxynucleotide method of RNA
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
     SEQUENCE FROM N.A., AND REVISIONS TO 53-59
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PDB; 10RS; x-ray; A=1-106.
PDB; 25C8; x-ray; L=1-103.
MGD; MGI:96495; Igk-C.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003006; Ig_CH.
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PROSITE; PS00290; IG_MHC; 1.
3D-structure; Direct protein Elmmunoglobulin domain.
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| IRSK; X-ray; B/E=1-106.
| IKBS; X-ray; L=1-106.
| IKCR; X-ray; L=1-106.
| IKCS; X-ray; L=1-106.
| IKCS; X-ray; L=1-106.
| IKCV; X-ray; L=1-106.
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                                                                                                                           sequencing.";
Cell 15:1067-1075(1978).
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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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"A genomic gene encoding the b5 rabbit immunoglobulin kappa constant region: implications for latent allotype phenomenon.";
Proc. Natl. Acad. Sci. U.S.A. 81:1789-1793 (1984).
-!- MISCELLANBOUS: The CDNA from which this sequence was derived contains a terminator codon within the V-region coding region. The origin of this codon and of the differences between this and other sequenced b5 C regions are unclear. The cDNA clone was made using mRNA from trypanosome-infected b5-homozygous rabbits.
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MEDLINE=84041515; PubMed=6314281;
Bernstein K.E., Skurla R.M. Jr., Mage R.G.;
"The sequences of rabbit kappa light chains of b4 and b5 allotypes differ more in their constant regions than in their 3' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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23-0CT-1986 (Rel. 02, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Ig kappa chain b5 variant C region.
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106 AA;
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NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2; Steen M.L., Hellman L., Pettersson U.; Steen M.L., Hollman L., Petters of U.; "The immunoglobulin lambda locus in rat consists of two C lambda genes
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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7C71850205381751 CRC64;
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Gene 55:75-84(1987).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                      | InterPro; | PR003597; | 19-1ike. | | |
| InterPro; | IPR003597; | 19-ci. |
| InterPro; | IPR003597; | 19-ci. |
| InterPro; | IPR003065; | 19-ci. |
| InterPro; | IPR003065; | 19-ci. |
| InterPro; | InterPro; | 10-ci. |
| PR0031TE; | PS00395; | IG | INTE; | 1. |
| PR0S1TE; | PS00395; | IG | INTE; | 1. |
| InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | InterPro; | Int
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SWART; SM00407; 1921.
PROSITE; PS50815; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin C region; Immunoglobulin G omain.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 0.017; 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
12 lambda-2 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
              EMBL; X00032; -; NOT ANNOTATED_CDS
EMBL; K01363; AAA31355.1; -.
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HSSP; P01842; 2MCG.
                                                                                                                                                                                                                                                                                                                                                        104 AA; 11079 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                    26.78;
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 26.7%
hes 28; Conservative
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                                                                                                                                                                                                                                                                                               85
104
                                                           PIR; A02124; KSRBV,
HSSP; P01837; 25C8.
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104
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                                                                                                                                                                                                                                                                                                    3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
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                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heidmann O., Rougeon P.;
"Multiplicity of constant kappa light chain genes in the rabbit genome: a b4b4 homozygous rabbit contains a kappa-bas gene.";
genome: a b4b4 homozygous rabbit contains a kappa-bas gene.";
-1- MISCELLANEOUS: In Basilea rabbits, the major type of light chain is lambad. The kappa chain shown is a minor component. All other rabbit B allotyges have Cys-64.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Indels 12; Gaps
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Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                       . 9
                                                                                                                                                                                                                                                                                                                                                                                                                  63 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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                                                                                                                                       Query Match
17.0%; Score 99; DB 1; Length 104;
Best Local Similarity 21.5%; Pred. No. 0.052;
Matches 23; Conservative 28; Mismatches 50; Indels
                                                          Interchain (with heavy chain) F087906DE43F7276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 106;
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Pfam; PF00047; ig; 1.
PROSITE; PS50815; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; FALSE_NEG.
Immunoglobulin C region; Immunoglobulin domain.
NON_TER
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21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Ig kappa-b4 chain C region.
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Best Local Similarity 29.4%; Pred. No.
Marches 32; Conservative 21; Mismatches
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PIR, A0121; K4RBS.
MSSP, P01837; 2528
INCERPC; IPRO07110; IG-like.
InterPro; IPRO03006; IG_MHC.
99 IG
85
103 In
11318 MW;
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3 PVA-PSVLLEPPSKEE--LTTGTATIVCVANKFYPSD--ITVTWKVDGTTQQSGIENSKT 57
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Search completed: November 17, 2005, 07:52:15 Job time: 79.1461 secs

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TYPE: amino acids
TOPOLOGY: linear
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6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-232-246A-21
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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: FIGHER, Phillip M.

TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

TITLE OF INVENTION: CONJUGATES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Learington

STATE: MA

COUNTRY: USA
Sequence 40, Sequence 26, Sequence 26, Sequence 28, A Sequence 8, A Sequence 8, A Sequence 8, A Sequence 8, A Sequence 9, A Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 14, A Sequence 13, Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequence 14, A Sequ
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/44,644
FILING DATE:
CLASSIFICATION NUMBER: US/08/444,644
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTOMENY/AGENT INFORMATION:
                                                           US-08-444-644-26
US-08-232-246A-26
US-08-422-010-8
US-08-422-092-8
US-08-788-800-5
US-08-788-800-5
US-08-788-800-5
US-08-788-800-5
US-09-301-593-20
US-08-313-942-13
US-08-378-939-42
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US-08-024-253-8
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; Sequence 30, Application US/08444644
Partent No. 6015555
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK
TELECOMMUNICATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                  1006
1007
1007
1007
1008
1009
1009
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Phillip M.
TRANSFERRIN RECEPTOR SPECIFIC
ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
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                                                                                                                            61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                             61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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95.3%; Pred. No. 5.9e-55;
ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 086/232,246
FILING DATE: 07-JUL-1994
FRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         Sequence 21, Application US/08444644
Patent No. 6015555
GENERAL INPORMATION:
TITLE OF INVENTION: TRANSFERRIN REC
TITLE OF INVENTION: ANTIBODY-NEURO;
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALE
TELECOMMUNICATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 110 amino acids
amino acid
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; FRAGMENT TYPE: internal
US-08-444-644-21
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Best Local Similarity
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CITY: Lexington
STATE: MA
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Betent No. 6239508
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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                                                                                                                  Length 109;
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                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC-DOS/MS-DOS
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1999
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1999
ATCORNEY/AGENT INFORMATION:
NAME: WAGNEY: Richard W:
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: 31,480
REGIS
                                                                                                                  Score 554; DB 3;
Pred. No. 2.4e-56;
5; Mismatches 2;
                                                                                                               95.4%;
                                                                                                               Query Match
Best Local Similarity 93.6
Matches 102; Conservative
      protein
internal
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internal
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GY: linear
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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-444-644-30
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FRAGMENT TYPE:
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US-08-232-246A-30
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RESULT 6
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                                                                                    GENERAL INFORMATION:

APPLICANT: Friden, Phillip M.

TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

TITLE OF INVENTION: CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                         NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/23,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
ATTONEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERNCE/DOCKET NUMBER: ALK88-15AAA
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                               Sequence 21, Application US/08232246A
Patent No. 6329508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-232-539D-60

Sequence 60, Application US/08232539D

Patent No. 5965709

GENERL INFORMATION:
APPLICANT: Presta, Leonard G.

APPLICANT: Jardieu, Paula M.
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Best Local Similarity 95.33
Matches 101, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
RESULT 4
US-08-232-246A-21
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1 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 60
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Squence 4, Application US/08070116A

Squence 4, Application US/08070116A

Patent No. 5885573

GENERAL INFORMATION:

APPLICANT: Joinin, Robert A.

APPLICANT: Joiliffe, Linda K.

APPLICANT: Joiliffe, Linda K.

APPLICANT: Joiliffe, Linda K.

APPLICANT: Joiliffe, Linda K.

TITLE OF INVENTION: Methods and Materials For Modulation

TITLE OF INVENTION: Toxicity of Monoclonal Antibodies

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSE: Arnold, White & Durkee

STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.1%; Score 541; DB 2; Length 105; Best Local Similarity 97.1%; Pred. No. 7.2e-55; Matches 101; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSE: 6 Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 21-Apr-1994
CLASSIFICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: SVOBOGA, CTalig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 99,044
REFERENCE/DOCKET NUMBER: 99,044
REFERENCE/DOCKET NUMBER: 99,044
REFERENCE/DOCKET NUMBER: 99,044
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COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 105 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-232-539D-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COPOLOGY:
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65

Gaps

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4 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phillip M.
TRANSFERRIN RECEPTOR SPECIFIC
ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                            Score 540; DB 4; Length 109;
Pred. No. 9.9e-55;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34,480
REFRERENCE DOCKET NUMBER: ALK88-15AAAZ
TELECOMUNICATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 424

RIOR APPLICATION 1424

PRIOR APPLICATION DATE:
FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATE: 07-JUL-1994

PRIOR APPLICATION DATE: 07/800,458

FILING DATE: 26-NOV-1991

PRIOR APPLICATION NUMBER: PCT/US90/05077

FILING DATE: 07-SEP-1990

PRIOR APPLICATION NUMBER: BCT/US90/05077

FILING DATE: 07-SEP-1990

PRIOR APPLICATION NUMBER: US 07/404,089

FILING DATE: 07-SEP-1980

ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44, Application US/08444644
Patent No. 6015555
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.3%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Wagner, Richard W. REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Friden, Phill
TITLE OF INVENTION: ANTI:
TITLE OF INVENTION: CONJUITIE OF INVENTION: CONJUITIE OF INVENTION: CONJUITIE OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-050-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02173
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APPLICANT: Bluestone, Jeffrey A.
APPLICANT: Bluestone, Jeffrey A.
APPLICANT: Zivin, Robert A.
APPLICANT: Joiliffe, Linda K.
TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.9%; Score 540; DB 2; Length 109; 95.3%; Pred. No. 9.9e-55; ive 3; Mismatches 2; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,050
FILING DATE: Concurrently Herewith
CLASSIFICATION NUMBER: PCT/US94/06198
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06198
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/070,116
FILING DATE: 01-JUN-1993
ATTORNEY/AGENT INFORMATION:
              OPERATING SISTEM: EC-LOST MOST OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE 
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REFERENCE/DOCKET NUMBER: ARCD:208
TELECOMMUNICATION INFORMATION:
          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 4, Application US/08557050 ; Patent No. 6491916
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Texas
COUNTRY: U.S.
ZIP: 77210
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US-08-557-050-4
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SEQUENCE CHARACTERISTICS
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FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Phillip M.
TRANSFERRIN RECEPTOR SPECIFIC
ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
                                                                                                                    Gaps
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                                                                                                                                                                                                                                  QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                        Score 540; DB 3; Length 110;
Pred. No. 1e-54;
3; Mismatches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FLING DATE: 04-MAY-1994
CLASSIFICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 540; DB 3;
Pred. No. 1e-54;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERNCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMINICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                        Sequence 44 Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
    TITLE OF INVENTION: TRANSFERRIN RECE
; TITLE OF INVENTION: ANTIBODY-NEUROPH
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith (STREET: Two Militia Drive
                                                                            92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.9%;
95.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 amino acids
                                                                        Query Match 92.9
Best Local Similarity 95.3
Matches 101; Conservative
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Best Local Similarity 95.3
Matches 101; Conservative
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internal
                        internal
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; MOLECULE TYPE:

; FRAGMENT TYPE:
US-08-444-644-44
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FRAGMENT TYPE:
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VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE

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4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
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                                                                                                                                                                                                                                                                                                                                   Phillip M.
TRANSFERIN RECEPTOR SPECIFIC
ANTIBOY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                            64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                               65 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Pred. No. 3.5e-52;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR 17TILE OF INVENTION: CONJUGATES NUMBER OF SEQUENCES: 46 CORRESPONDENCES: 46 CORRESPONDENCES: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REPERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         Sequence 38, Application US/08444644
Patent No. 6015555
GENERAL INFORMATION:
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Best Local Similarity 91.5%;
Matches 97; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 3
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internal
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STATE: PA
COUNTRY:
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Sequence 38, Application US/08232246A

Patent No. 6329508
GENERAL INFORMATION:
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSES: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible .
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US 07/800,05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATPONENT/APANION: AAPPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATPONENTY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMUNICATION INFORMATION:
TELEPAN: (617) 861-6240
ITELEPAN: (617) 861-6240
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 110 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-08-569-147-85
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Sequence 85, Application US/08569147
Patent No. 6180377
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANISED ANTIBODIES

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Patent No. 6734287

GENERAL INOFMATION:

APPLICANT: Lawton, Robert

APPLICANT: Francoeur, Greg

TITLE OF INVENTION: Specific Binding Protein for Treating

TITLE OF INVENTION: Canine Allergy

FILE REFERENCE: 01-1275A

CURRENT APPLICATION NUMBER: US/09/281,760E

CURRENT FILING DATE: 1999-03-30

PRIOR APPLICATION UNMBER: 09/058,331

PRIOR FILING DATE: 1998-04-09
                                                                                                                                                                                                                                                                                                                                                                    OPERALIUS SYSIEM: KC-LUCS/MS-LUCS
SOFTWARE: PACENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,147
FILING DATE: 25-March-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Trujilo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: 35,719
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
SELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6180377ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (136)..(136)
OTHER INFORMATION: "n" stands for any nucleic acid
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
LENGTH: 107
                                                                                                                                                                                                    ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.8%;
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.7%; Score 166.5; DB 2
34.3%; Pred. No. 1.3e-11;
live 22; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08466163B
PAtent No. 6229509
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0/18P2C101
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
SEQ ID NO 1
LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Mismatches
                     CURENT APPLICATION DATA:
APPLICATION NUMBER:
ILING DATE: 21-Apr-1994
CLASSIFICATION NTO: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SVODOGA, Craig G.
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
RECISTRATION NUMBER: 39,044
RECISTRATION NUMBER: 39,044
RECISTRATION NUMBER: 39,044
REPERPONE: 650/225-1489
                                           UMBER: US/08/232,539D
21-Apr-1994
     WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 106 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 34.38
Marches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 34.39
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-232-539D-54
     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-466-163B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.1%; Score 175; DB 4; Length 107; Best Local Similarity 35.0%; Pred. No. 1.3e-12; Matches 36; Conservative 23; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 NGTITVTSTLPVNTNDWIEGETYYCRVTHPHLPKDIVRSIAKA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 108
                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (460)..(462)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (500)..(500)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (530)..(530)
OTHER_INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (853)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
LOCATION: (413)...(414)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                        NAME/KEY: misc feature
LOCATION: (451)..(451)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (847)..(849)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (1382)..(1382)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (1832)..(1832)
OTHER INFORMATION: "n" stands for any nucleic acid
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: IGE Antagonists
CORRESPONDENCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54. Application US/08232539D Patent No. 5965709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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US-08-232-539D-54
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Db 65 NGTLTVTSTLPVGTRDWIEG-ETQCRVTHPHLPRALMRSTTK 105

orh countleted. Movember 17 2006 07.52.66

Search completed: November 17, 2005, 07:53:55 Job time: 24.3927 secs

Sequence Sequence Sequence Sequence

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220, App 14, Appl 11, Appli 22, Appli 22, Appl 21, Appli 21, Appl 224, Appl 80, Appl 80, Appl 80, Appl 80, Appl 80, Appl 813, Appl 814, Appl 815,

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence

322, App 92, Appl 5, Appli 6, Appli 25, Appli

Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Perfect score:

Sequence:

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Scoring table:

Searched:

Database

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Sequence 11, Application US/10959318
| Publication No. US20050215768A1
| GENERAL INFORMATION:
| APPLICANT: Armour, Kathryn L
| APPLICANT: Clark, Michael R
| TITLE OF INVENTION: Polypeptides including modified constant regions
| TITLE OF INVENTION: Polypeptides including modified constant regions
| TITLE OF INVENTION: 99-302
| CURRENT FILING DATE: 2004-10-07
| CURRENT FILING DATE: 2004-10-07
| PRIOR FILING DATE: 2004-10-07
| PRIOR FILING DATE: 2003-10-17
| NUMBER OF SEQ ID NOS: 27
| SEQ ID NO 11
| LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.6%; Score 573; DB 18; Length 109; 99.1%; Pred. No. 1.9e-48; ive 0; Mismatches 1; Indels
US-10-627-556-270
US-10-959-318-17
US-11-018-102-23
US-11-018-102-23
US-11-018-102-25
US-10-207-655-220
US-10-627-556-12
US-10-1018-102-22
US-10-959-318-21
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US-10-959-318-21
US-10-627-556-294
US-10-627-556-294
US-10-627-556-292
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US-10-627-556-302
US-10-627-556-32
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Matches 108; Conservative
     US-10-959-318-11
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Sequence 12, Appl
Sequence 9, Appli
Sequence 16, Appl
Sequence 15, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 13, Appl
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Appli
                                                                                                                                                                                                Search time 82.3721 Seconds (without alignments) 553.666 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                     1 APPVAGPSVFLFPPKFKDTL......CKVSNKGLPSSIEKTISKAK 109
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1: \cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/NEW_PUB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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18: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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11: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-959-318-14
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 110
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Gaps

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APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTKP

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Sequence Sequence S

25 43 7 110 8 7

Score

Result Š

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OTHER INFORMATION: Variant of Human 1gG1 CH2 sequence with delta a, c and e (E268) OTHER INFORMATION: mutations
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RORANISM: Artificial Seguence
FEATURE:
OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b and d (D268)
OTHER INFORMATION: mutations
                                                           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK 60
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                          1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
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                                                                                                                                                                                                                                                                          Sequence 10, Application US/10959318

Sequence 10, Application US/10959318

Publication No. US20050215768A1

GENERAL INPORMATION:

APPLICANT: Armour, Kathryn L

APPLICANT: Clark, Michael R

TITLE OF INVENTION: POLYPeptides including modified constant regions

FILE REFERENCE: 39-302 10959,318

CURRENT FILING DATE: 2004-10-07

PRIOR APPLICATION NUMBER: PCT/GB2004/004254

PRIOR APPLICATION NUMBER: PCT/GB2004/004254

PRIOR APPLICATION NUMBER: GB324368.0

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.3

SEQ ID NO 10

LENGTH: 110

TYPE: PRT

ORGANISM: Artificial Sequence
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Publication No. US20050215768A1

GENERAL INFORMATION:

APPLICANT: Armour, Kathryn L

APPLICANT: Clark, Michael R

TITLE OF INVENTION: Polypeptides including modified constant regions

FILE REPERENCE: 39-302

CURRENT APPLICATION NUMBER: US/10/959,318

CURRENT FILING DATE: 2004-10-07

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-17

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.3

SEQ ID NO 15

LENGTH: 109
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                                                                                                                           60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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96.8%; Score 562.5; DB
Best Local Similarity 98.2%; Pred. No. 2e-47;
Matches 108; Conservative 0; Mismatches
                                                                                                                                                                                                                                                       RESULT 4
US-10-959-318-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Variant of Human 1gG1 CH2 sequence with delta a, b and e (E268); OTHER INFORMATION: mutations
US-10-959-318-12
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                                                                                                           RESULT 2
US-10-959-318-12
| Sequence 12, Application US/10959318
| Sequence 12, Application US/10959318
| Publication No. US20050215768A1
| GENERAL INFORMATION:
| APPLICANT: Armour, Kathryn L
| APPLICANT: Clark, Michael R
| TITLE OF INVENTY PELICATION NUMBER: US/10/959,318
| CURRENT APPLICATION NUMBER: US/10/959,318
| PRIOR PILING DATE: 2004-10-07
| PRIOR PILING DATE: 2004-10-07
| PRIOR FILING DATE: 2003-10-17
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: PatentIn version 3.3
| SEQ ID NO 12
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| Publication No. US2050215768A1
| GENERAL INFORMATION:
| APPLICANT: Armour, Kathryn L
| APPLICANT: Clark, Michael R
| TITLE OF INVENTION: Polypeptides including modified constant regions
| TITLE OF INVENTION: DOLYPEPTION NUMBER: US/10/959,318
| CURRENT APPLICATION NUMBER: US/10/959,318
| CURRENT APPLICATION NUMBER: PCT/GE2004/004254
| PRIOR APPLICATION NUMBER: G80324368.0
| PRIOR FILING DATE: 2004-10-07
| PRIOR FILING DATE: 2003-10-17
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 9
| LENGTH: 110
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                          REEQYNSTYRUVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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Pred. No. 1.9e-48;
0; Mismatches 1;
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.1%;
Matches 108; Conservative
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ORGANISM: Artificial Sequence
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Matches 108; Conservative
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US-10-959-318-9
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Length 109; Indels

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OTHER INFORMATION: Variant of Human 1gG1 CH2 sequence with delta c and d (D268) OTHER INFORMATION: mutations
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Sequence 13, Application US/10959318

Sequence 13, Application WS/10959318

BENERAL INFORMATION:
APPLICANT: Armour, Kathryn L
APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302
CURRENT FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-10-17
PRIOR FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 13

LENGTH: 110
                                                                                                                                                                                                                      1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
TITLE OF INVENTION: Polypeptides including modified constant regions
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: PCT/GB2004/004254
PRIOR FILING DATE: 2004-10-07
PRIOR PLING DATE: 2003-10-17
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                                                                                                         Score 554; DB 18;
Pred. No. 1.4e-46;
5; Mismatches 2;
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Pred. No. 4.8e-46;
1; Mismatches 3;
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Publication No. US20050215768A1
GENERAL INFORMATION:
                                                                                                         Query Match 95.4%;
Best Local Similarity 93.6%;
Matches 102; Conservative
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Best Local Similarity 95.5%;
Matches 105; Conservative
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  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-318-2
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                                                                                                                                                               1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                               1 APPVAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTKP 60
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Publication No. US20050215768A1

Sequence 16, Application US/10859318

Publication No. US20050215768A1

SEQUENCE INFORMATION:

APPLICANT: Armour, Kathryn L

APPLICANT: Armour, Kathryn L

APPLICANT: ATILE OF INVENTION: Polypeptides including modified constant regions

TITLE OF INVENTION: Polypeptides including modified constant regions

CURRENT APPLICATION NUMBER: US/10/959,318

CURRENT FILING DATE: 2004-10-07

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.3

SEQ ID NO 16

LENGTH: 109
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APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
TITLE OF INVENTION: 99-302
CURRENT EXPERIENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT APPLICATION NUMBER: PG7/GB2004/004254
PRIOR APPLICATION NUMBER: PG7/GB2004/004254
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
SEQ ID NOS: 27
LENGTH: 109
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                                                   Length 109;
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                                                                                                         Indels
                                                Score 559; DB 18;
Pred. No. 4.4e-47;
1; Mismatches 3;
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                                                      96.2%;
96.3%;
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ORGANISM: Artificial Seguence
                                                Query Match
Best Local Similarity 96.3
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 96.3
Matches 105; Conservative
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US-10-959-318-15
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US-10-959-318-2
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RESULT 12
US-10-627-556-270
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US-10-959-318-17
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Best Local S
Matches 102
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                                                                                                        OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and e (E268) OTHER INFORMATION: mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and d (Q268) OTHER INFORMATION: mutations
                                                                                                                                                                                                                                                                                                            1 APPVAGGPSVFLFPPKPTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTK 60
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Publication No. US20050215768A1

GENERAL INFORMATION:

APPLICANT: Clark, Michael R

TITE OF INVENTON:

FILE REFERENCE: 39-30.

CURRENT APPLICATION NUMBER: US/10/959,318

CURRENT APPLICATION NUMBER: PCT/GB2004/004254

PRIOR APPLICATION NUMBER: PCT/GB2004/004254

PRIOR PILING DATE: 2004-10-07

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                        1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                             Gaps
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Sequence 8, Application US/10959318

Sequence 8, Application No. US20050215768A1

Sequence 9, US20050215768A1

GENERAL INPORMATION:
APPLICANT: Clark, Michael R

APPLICANT: Clark, Michael R

TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302

FULE REFERENCE: 20-410-07

CURRENT FILING DATE: 2004-10-07

PRIOR APPLICATION NUMBER: PCT/GB2004/004254
                                                                                                                                                                                                                                                                                                                                                                                                 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                                                                                                                                                                               DB 18; Length 110;
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                                                                                                                                                                                               Score 548.5; DB 18; Length
Pred. No. 4.8e-46;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 548; DB 18;
Pred. No. 5.3e-46;
1; Mismatches 2;
                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                               Query Match
Best Local Similarity 95.5%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 97.2%;
Matches 103; Conservative
                                                                                                                                                    US-10-959-318-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 7
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-10-959-318-7
SEQ ID NO 14
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TYPE: PRT
PREADURS: Artificial Sequence
FEATURE:
OTHER INFORMATION: Wariant of Human IgG1 CH2 sequence with delta a and e.(E268)
OTHER INFORMATION: mutations
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PUBLICATION NO. US20050136049A1

SEQUENCE 1 NFORMATION:

APPLICANT: LEDBETTER, JEFFREY A.

APPLICANT: HAYDEN-LEDBETTER, MARTHA

APPLICANT: HAYDEN-LEDBETTER, MARTHA

TITLE OF INVENTION: BTER A.

TITLE OF INVENTION: BTER A.

TITLE OF INVENTION: BY SET BY A.

FILE REFERENCE: 49076.000004.CIP2

CURRENT APPLICATION NUMBER: US/10/627,556

PRIOR APPLICATION NUMBER: 10/053,530

PRIOR PILING DATE: 2002-01-17

PRIOR PILING DATE: 2002-01-17

PRIOR PILING DATE: 2002-01-16

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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ilarity 96.2%; Pred. No. 6.6e-46;
Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
PRIOR FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: GB0324368.0
PRIOR FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
SEQ ID NO 8
LENGTH: 110
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ORGANISM: Artificial sequence
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nes 102; Conserv
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Sequence 23, Application US/11018102.
Publication No. US20050136061A1
Publication No. US20050136061A1
APPLICANT: Centocor, Inc.
TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CENGO45 USA NP
CURRENT APPLICATION NUMBER: US/11/018,102
CURRENT FILING DATE: 2004-12-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.7%; Score 544.5; DB 20; ilarity 94.5%; Pred. No. 1.2e-45; Conservative 1; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: engineered G1 CH2 US-11-018-102-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 104; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                             SEQ ID NO 23
LENGTH: 110
TYPE: PRT
                               RESULT 15
JS-11-018-102-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Variant of Human 19G2 CH2 sequence with delta d (D268) mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Variant of Human IgG2 CH2 sequence with delta e (E268) mutation
US-10-959-318-18
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                                                                   APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-30.
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT APPLICATION NUMBER: US/10/959,318
FILOR FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: PGT/GB22004/004254
PRIOR PRILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
SEQ ID NO 17
LINGTH: 109
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APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT PILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
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94.0%; Score 546; DB 18; Length 109;
Best Local Similarity 92.7%; Pred. No. 8.3e-46;
Matches 101; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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94.0%; Score 546; DB 18;
Best Local Similarity 92.7%; Pred. No. 8.3e-46;
Matches 101; Conservative 5; Mismatches 3;
Sequence 17, Application US/10959318
Publication No. US20050215768A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/10959318; Publication No. US20050215768A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-959-318-18
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LENGTH: 109
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Gaps

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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- protein search, using sw model OM protein Run on:

November 17, 2005, 06:38:35; Search time 90.8333 Seconds (without alignments) 464.112 Million cell updates/sec

US-09-674-857-2

1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKTK 109 Sequence:

Perfect score:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed sed 08 08 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	æ			SUMMAKLES	
Score	Query e Match	/ h Length	DB	ID	Q,
580	0 100.0	0 326		ADF77155	Adf77155 Anti-VAP-
580		0 447	æ	ADQ17121	Adq17121 Humanised
58	0 100.0	0 462	æ	ADF77154	Adf77154 Chimeric
577		5 436	7	ADM33853	Adm33853 Human HuE
577		4	8	ADR48984	Adr48984 HuEPO-L-F
577		4	7	ADM33376	Adm33376 Human GCS
572	σ		7	AAR41709	Aar41709 Undefined
572	2 98.6		m	AAY54997	Aay54997 Mutated C
572	2 98.6		ო	AAB07476	
57	σ		4	AAB76423	Aab76423 Human IgG
572			4	AAB67203	Aab67203 Human IgG
57			ហ	AAG78434	Aag78434 Native se
572			9	ABR42440	Abr42440 Human 1gG
572		5 217	æ	ADH75378	Human
57			'n	ABG31095	Human
5,			8	ADR48993	Adr48993 Human IgG
57			æ	ADS84436	Ads84436 Human ant
57			œ	ADR68578	Adr68578 Human ant
57			4	AAE02643	Aae02643 Human imm
572			'n	AAM47857	Aam47857 Human Ig-
57	σ		Ŋ	ABG30462	Human
572			Ŋ	ABG77148	Abg77148 Anti-IGF-
572	Q		φ	AAE32916	Aae32916 Human imm
57	2 98.6	326	9	AAE32628	Aae32628 Human imm
572	σ	326	ø	AA030894	Aao30894 Human imm

5 7 ADE97353 5 8 ADM41541 5 8 ADM41541 6 8 ADM59469 6 8 ADR26785 1 2 AAX26782 2 AAX26782 2 AAX26782 2 AAX86782 4 AAB67322 4 AAB67322 4 AAB67322 4 AAB67323 2 AAX31670 3 2 AAX31670 5 8 ADK52396 6 ADK52396 7 ADM8320 8 ADK52396 8 ADK52396 8 ADK52396 8 ADK52396 8 ADK52396 9 ADK52312 9 AAX93734		7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		Adm18320 Human CD4 Aay93734 The heavy
		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ADE97353 ADF75002 ADM41411 ADM95469 ADR28562 AAR2678 AAR2678 AAR8678 AAR8678 AAB67322 AAB67322 AAB72230 AAR72230 AAR72230 AAK52330 AAK52332 AAK52332	ADM18320 AAY93734
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ALIGNMENTS

complementarity determining region; CDR; mouse; Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain; chimeric; inflammatory disorder; rheumatoid arthritis; inflammatory bowel disease; autoimmune disease; psoriasis; immunoscintigraphic imaging. Anti-VAP-1 monoclonal antibody H chain constant region. ADF77155 standard; protein; 326 AA. (first entry) 26-FEB-2004 ADF77155;

Homo sapiens

WO2003093319-A1.

13-NOV-2003.

28-APR-2003; 2003WO-FI000330.

29-APR-2002; 2002FI-00000807.

(BIOT-) BIOTIE THERAPIES CORP.

Clark MR; Laukkanen M, Salmi M, Jalkanen S,

WPI; 2004-022642/02.

New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and encoding nucleic acid molecules, useful for diagnosing and treating chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.

Claim 18; SEQ ID NO 16; 56pp; English.

This sequence represents the constant region of a human anti-Vascular Adhesion Protein-1 (VAP-1) antibody heavy chain. This sequence may be used in the production of a chimeric mouse-human anti-VAP-1 antibody. The nucleic acid molecules, polypeptides or antibodies are useful in treating VAP-1 mediated inflammatory disorders, such as rheumatoid arthritis, inflammatory bowel disease, autoimmune diseases or psoriasis. The chimeric VAP-1 antibody is further used for in vitro and in vivo chimeric applications, including in vivo immunoscintigraphic imaging of inflammation sites. The chimeric MAD's of the invention have improved kinetic properties compared to the corresponding murine antibodies.

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26-FEB-2004
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                                                                             pain, or f
arthritis.
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'note= "Extended CDR (complementarity determining region)
                                                                                                                                                                                                                                                                                                                                                                        /note= "Extended CDR (complementarity determining region)
                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Wild-type Ile of murine Mab 911 substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Wild-type Met of murine Mab 911 substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild-type Gly of murine Mab 911 substituted by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Wild-type Leu of murine Mab 911 substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                murine Mab 911 substituted by
                                                                 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                     nerve growth factor; anti-NGF antibody; El3.5 trigeminal neurone; analgesic; immunomodulator; post-surgical pain; rheumatoid arthritis; osteoarthritis; inflammatory cachexia; gene therapy; monoclonal antibody 911; humanised antibody E3; heavy chain; murine;
                                                 Gaps
                                                                                                                                                                                                                                   Humanised anti-NGF antibody E3 heavy chain full-length protein.
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                                                                                                                   REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 219
                                                                                                        REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                              Length 326;
                                                0; Indels
                            Score 580; DB 8;
Pred. No. 9e-51;
                                             Mismatches
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                                                                                                                                                                          ADQ17121 standard; protein; 447 AA
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                            100.0%;
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28-JAN-2003; 2003US-0443522P.
08-OCT-2003; 2003US-0510006P.
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                                                                                                                                                                                                                (first entry)
                                                Conservative
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                           Query Match
Best Local Similarity
Matches 109; Conserv
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          Sequence 326 AA;
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o sapiens.
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                                                                                                                                                                                                                                                                                                                                 Synthetic.
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The invention relates to a novel anti-nerve growth factor (NGF) antibody which binds NGF with a KD of less than about 2 nM and inhibits human NGF-dependent survival of mouse E13.5 trigeminal neurones with an ICSO of about 100 or 10 pM or less, where the ICSO is measured in the presence of emonstrates analgesize and immunomodulator activities and may be useful commonstrates analgesize and immunomodulator activities and may be useful for preventing analgesize in immunomodulator activities and may be useful for preventing and/or treating pain, including post-surgical pain and pain associated with rheumatoid arthritis or osteoarthritis. The antibody may be further utilised for treating inflammancory cachexia associated current sequence is that of the humanised anti-NGF antibody E3 heavy chain full-length protein of the invention which was synthesised via gratting CDRs (complementarity determining regions) from murine anti-NGF mab (monoclonal antibody) 911 onto human framework sequences and subsequently mutating the CDRs to improve binding.
                                                                                                                                New anti-nerve growth factor antibodies for preventing or treating pain, including post-surgical pain, rheumatoid arthritis pain or osteoarthritis pain, or for treating inflammatory cachexia associated with rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVOFNWYVDGVEVHNAKTKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 447;
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Pred. No. 1.3e-50;
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100.0%; Pred. No. 1...
... 0; Mismatches
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  Rosenthal A;
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Best Local Similarity 100.
Matches 109; Conservative
  Pons J,
                                                   2004-525786/50
                                                                               N-PSDB; ADQ17170
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Shelton DL,
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                                                                                                                   This sequence represents a chimeric human-mouse anti-Vascular Adhesion Protein-1 (VAP-1) antibody heavy chain. This sequence may be used in the production of a chimeric mouse-human anti-VAP-1 antibody. The nucleic acid molecules, polypeptides or antibodies are useful in treating VAP-1 mediated inflammatory disorders, such as rheumatoid arthritis, inflammatory bowel disease, autoimmune diseases or psoriasis. The chimeric VAP-1 antibody is further used for in vitro and in vivo diagnostic applications, including in vivo immunoscinitigraphic imaging of inflammation sites. The chimeric WAP's of the invention have improved kinetic properties compared to the corresponding murine antibodies.
                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                               New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and encoding nucleic acid molecules, useful for diagnosing and treating chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.
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fragment crystallisation region; FC; chronic anaemia; renal disease;
cancer chemotherapy; rheumatoid arthitis; AIDS;
myelodysplastic syndrome; (HuEPO)-L-vPcgamma2; human.
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                                                                                                                                                                                                                                                                                                                                                     307 REEQFINITERVYSVLTVVHQDMLNGKEYKCKVSNKGLPSSIEKTISKTK 355
                                                                                                                                                                                                                                                                                                                                         61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                         Length 462;
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                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                        100.0%; Score 580; DB 8; 100.0%; Pred. No. 1.4e-50;
           Laukkanen M, Clark MR;
                                                                                                                                                                                                                                                                              Mismatches
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/note= "Signal peptide"
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                                                                                                 Claim 9; SEQ ID NO 15; 56pp; English
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/note= "IgG2 Fc"
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/note= "Linker"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "EPO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                             Matches 109; Conservative
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           Salmi M,
                             WPI; 2004-022642/02
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                                       N-PSDB; ADF77144
                                                                                                                                                                                                                                      Sequence 462 AA;
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Synthetic.
           Jalkanen S,
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The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFC fusion protein comprising HuBPO, a peptide linker, and a human comprising HuBPO, a peptide linker, and a human community of fragment crystallisation region) variant. Also included is a carbohydrate-derived cell line producing the human crospinal protein exhibits an enhanced in vitro biological activity of at least 2-fold relative to that of recombinant HuBPO on a molar of at least 2-fold relative to that of recombinant HuBPO on a molar of at least 2-fold relative to that of recombinant HuBPO on a molar of acids is present between HuBPO and the human IGG FC variant comprises a hinge, CH2 and CH3 domains of human IGG FC contains amino acid mutations to attenuate effector functions. The human CG TG FC variant comprises a hinge, CH2 and CH3 domains of human IGG with Pro3131ser mutation, human IGG with Ser228Pro and Leu233Ala mutations, or human IGG1 with chronic anaemia caused by renal failure, cancer crecombinant human erythropoietin-L-vFC fusion proteins are useful for treating patients with chronic anaemia caused by renal failure, cancer chemotherapy, rheumatoid arthritis, azathioprine treatment for H1V creating patients with chronic anaemia caused activity and prolonged presence of the human erythropoietin-L-vFC fusion protein in the serum, as compared to prior art, leads to lower dosages and less frequent injections result in better patient compliance and quality of life. The present sequence represents the fusion protein HuBPO-L-vFGgamma2.
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                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant human erythropoietin-L-vFc fusion proteins, useful for treating patients with chronic anemia caused by renal failure, cancer chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REEQFINSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPASIEKTISKTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.5%; Score 577; DB 7;
99.1%; Pred. No. 2.6e-50;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR48984 standard; protein; 436 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 2A; 14pp; English
17-AUG-2001; 2001US-00932812.
                                                                                                                                                                                                                                                     Sun CRY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                   WPI; 2003-616080/58.
                                                                                 CBE
RR.
KC.
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                                                                                                                                                                                                                                                     Sun BNC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 436 AA;
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Synthetic

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21-JAN-2004; 2004US-00761593
                 17-AUG-2001; 2001US-00932812
                              Sun CRY;
                                  2004-634851/61.
                     CBK.
                              Sun BNC,
                                  WPI; 2004-634851,
N-PSDB; ADR48983
    US2004175824-A1
                     NS S
        09-SEP-2004
                     (SUNL/)
(SUNB/)
(SUNC/)
                              Sun LK,
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CHERON, a peptide linker, and a human 1gG FC variant, is new.
INDEPRINERY CLAIMS are also included for the following: a chinese hammeer of CHERO), a peptide linker, and a human 1gG FC variant, to have fusion protein in its growth medium in access of 10 Emicro; g per million cells in a 24 hour period; and a method for making a recombinant thrisin protein comprising the Protein.

CC Gravid, and a method for making a recombinant thrisin protein comprising the Protein. The peptide linker containing 20 or fewer amino acids selected from glycine, serine, alanies and threomine. The between Hubbo and the human 1gG FC variant, and the domprises two or more amino acids selected from glycine, serine, alanies of human 1gG variant comprises a hinge, CR3, and CR3 domains of human 1gG variant comprises a hinge, CR3, and CR3 domains of human 1gG variant comprises a hinge, CR3, and CR3 domains of human 1gG variant comprises a hinge, CR3, and CR3 domains of human 1gG variant comprises a hinge, CR3, and CR3 domains of human 1gG variant comprises a hinge, CR3, and CR3 domains of human 1gG variant comprises a hinge, CR3, and CR3 domains of human 1gG variant comprises a hinge, CR3, and CR3 domains of human 1gG variant comprises a hinge, CR3, and CR3 domains of human 1gG variant comprises a hinge, CR3, and CR3 domains of human 1gG variant comprises a hinge, CR3, canded the human 1gG variant comprises a hinge, CR3, canded the human 1gG variant comprises a hinge cR3, domains of human 1gG variant comprises a hinge cR3, domains of human 1gG variant comprises a hinge cR3, domains of human 1gG variant comprises a linge critical manual activity similar to or higher than protein comprises generating a CR0-derived cell line variant comprises generating a CR0-derived cell line variant comprises generating a CR0-derived cell line variant comprises generating a CR0-derived cell line variant comprises generating a CR0-derived cell line variant comprises generating a CR0-derived cell line variant comprises generating a CR0-derived cell line varian New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin (HuEPO), a peptide linker, and a human IgG Fc variant, useful for treating chronic anemia due to renal diseases, cancer chemotherapy, or rheumatoid arthritis. Claim 3; SEQ ID NO 18; 31pp; English.

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and incorporates a BamHI site. The resulting DNA fragments of approximately 600 bp were inserted into a holding vector such as pUC19 at the HindIII and BamHI sites to give the pBPO plasmid. The sequence of the human EPO gene was confirmed by DNA sequencing.
                                                                                                                                                                            221 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 280
                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; immunostimulant; antianaemic; anti-HIV; protein therapy; human; granulocyte colony-stimulating factor; GCSF; GCSF-L-vFc; immunoglobulin 6; IgG; fargment of crystallisation; immune disorder; haematopoietic disorder; chemotherapy; leukaemia; anaemia; AIDS; bone marrow transplantation; chronic neutropeana; fusion protein; fragment of crystallisation gamma 2; Fc gamma 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mature human GCSF-L-fragment of crystallisation
                                                                                                                                                   1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Human GCSF-L-fragment of crystallisation gamma 2 fusion protein.
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                                                                                                                                                                                                                      281 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPASIEKTISKTK 329
                                                                                             Length 436;
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild type Pro substituted by Ser"
                                                                                            Score 577; DB 8; L. Pred. No. 2.6e-50; 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .30
/label= GCSF leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                    ADM33376 standard; protein; 448 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma 2 fusion"
331
                                                                                             Query Match
Best Local Similarity 99.1%;
Matches 108; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001; 2001US-00968362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2001; 2001US-00968362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sun LK, Sun BNC, Sun CRY;
                                                                                                                                                                                                                                                                                                                                                          (first entry)
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/note= "Ma
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(SUNB/) SUN B N C.
(SUNC/) SUN C R Y.
                                                                    Sequence 436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                               ADM33376;
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                                                                                                                                                                                                                                                                      RESULT 6
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New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-vFc fusion protein for treating immune or hematopoietic system disorders comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin G

WPI; 2003-585400/55.

N-PSDB; ADM33375

Disclosure; Fig 2A; 15pp; English.

variant

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The invention describes a recombinant human granulocyte colony-

stimulating factor (hG-CSF)-L-vFc fusion protein comprising hG-CSF, a

peptide linker, and a human immunoglobulin G (IGG) Fc variant. Also

described are: a CHO-derived cell line producing the above hG-CSF-L-vFc

fusion protein in its growth medium in excess of 10 £mgr;g per million

cells in a 24-hour period; and making the recombinant fusion protein

cited above, comprising generating a CHO-derived cell line cited above,

growing the cell line under conditions the recombinant fusion protein is

expressed in its growth medium, and purifying the expressed protein. The

recombinant fusion protein is useful in treating a variety of conditions

associated with an impaired immune or haemacopoietic system, including

cancer chemotherapy, leukaemias, anaemias, AIDS, bone marrow

transplantation, and chronic neutropenias. This is the amino acid

sequence of human GCSF-L-fragment of crystallisation gamma 2 variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 292
                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AlDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in AAR41707-09 are encoded by the expression vector pAH4625. This vector represents the cloning of the human gamma isotype,
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REEQFINSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                    Length 448;
                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                Score 577; DB 7;
Pred. No. 2.7e-50;
1; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Undefined ORF2 encoded by plasmid pAH4625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 17J; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR41709 standard; protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                      99.5%;
99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
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Best Local Similarity 99.1
Matches 108; Conservative
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                                                                                                                                                                                                                                                                                                                Sequence 448 AA;
                                                                                                                                                                                                                                                                              fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9310819-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUN-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR41709;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
       $$$$$$$$$$$$$$$$$$$$$$$
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gamma-2, with the variable region of the murine monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CHI. Git and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ43345), was transfected into SP2/0 cells and clones were isolated. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding molecule, CH2 sequence; complement dependent lysis, FogammaRIIb; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degramulation; phagocytosis; vasculitis; Crohn's disease; graft-vs-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopaenia; Goodpastures disease; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the mutated CH2 molecule G2deltaa, and is a binding molecule of the invention. The recombinant binding molecule is
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                             1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                             98.6%; Score 572; DB 2; Length 109; 98.2%; Pred. No. 1.6e-50; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sickle cell anaemia; coronary artery occlusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williamson LM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Fig 17; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence G2deltaa.
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                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.2
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-039075/03
                                                                                                                                                                                                                                                                                         Sequence 109 AA;
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dependent lyais, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant domain of a human immunoglobulin (G [160] heavy chain. The binding molecule is used to bind a target molecule (especially FegammaRID causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding molecule is useful for the treatment of graft-vs-binding of a second binding molecule is useful for the treatment of graft-vs-binding of a second binding molecule is useful for the treatment of graft-vs-binding of a second binding molecule is useful for the treatment of captured by the binding molecule is useful for the treatment of graft-vs-binding of a second binding molecule is useful for the treatment of captured captured by a second binding molecule is useful for the treatment of graft-vs-binding molecule is useful for the treatment of graft-vs-cautoimmune thrombocytopaenia, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, asthma and allergy), cetal/neonatal alloimmune thrombocytopaenia, asthma and allergy), cetal/neonatal alloimmune thrombocytopaenia, sickle cell anaemia and corronary artery occlusion). The binding molecules do not activate complement or trigger cytocoxic activities through FegammaR and desirable indenned maino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent being able to cross the human placenta through interaction with FeRn being able to cross the human placenta through interaction with FeRn being able to cross the human placenta through interaction with FeRn being able to cross the human placenta through interaction with FeRn being able to cross the human placent a through interaction with FeRn being able to cross the human placent a through interaction with FeRn being able to cross the manner and placent and the protein
    capable of binding a target molecule without triggering complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (neonatal Fc receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 109 AA;
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                                                                         1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                         1 APPVAGPSVFLFPPKPFDTLMISKTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
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                                                                                                                                            REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
     Score 572; DB 3; Length 109;
Pred. No. 1.6e-50;
0; Mismatches 1; Indels
 98.64;
99.14;
Query Match
Best Local Similarity 99.1
Matches 108; Conservative
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RESULT

Z AAB07476 standard; protein; 217

AAB07476;

(first entry) 20-OCT-2000

Amino acid sequence of native IgG Fc region humIgG2.

IgG antibody, light chain; Fc region; effector function; cancer; allergy; asthma; LFA-1-mediated disorder; tumour; cancer.

Homo sapiens

WO200042072-A2

20-JUL-2000.

14-JAN-2000; 2000WO-US000973

99US-0116023P. 15-JAN-1999;

(GETH) GENENTECH INC

Presta LG;

WPI; 2000-476035/41.

New Fc region-containing polypeptides that have altered effector function due to one or more amino acid modifications in the Fc region, useful in the treatment of cancer and allergic conditions such as asthma.

Disclosure; Fig 22A; 132pp; English

produce Fc region-containing polypeptides that have altered effector function as a consequence of one or more amino acid modifications in the Fc region. The variant polypeptides are useful for treating cancer, allergic conditions such as asthma (with an anti-lgE antibody), and LFA-mediated disorders. Where the polypeptide binds the HER2 receptor, the disorder preferably is HER2-expressing cancer, e.g. a benign or malignant tumour characterized by overexpressing cancer, e.g. a benign or malignant tumour characterized by overexpression of the HER2 receptor. Such cancers include breast cancer, gquamous cell cancer, small-cell lung cancer, non-small cell lung cancer, qastrointestinal cancer, pancreatic cancer, hepatoma, colon cancer, liver cancer, bladder cancer, hepatoma, carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck The proteins are used to AAB07474-78 represent native IgG Fc regions. cancer

Sequence 217 AA;

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                                                                              1 APPVAGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                   2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                           Gaps
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Query Match 98.6%; Score 572; DB 3; Length 217; Best Local Similarity 98.2%; Pred. No. 3.6e-50; Matches 107; Conservative 1; Mismatches 1; Indels
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RESULT 10 AAB76423

Ş AAB76423 standard; protein; 217

AAB76423;

(first entry) 10-APR-2001

Human 19G2 Fc region amino acid sequence.

Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Albaimer* disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.

sapiens. Homo

WO200101748-A2

11-JAN-2001.

30-JUN-2000; 2000WO-US018283.

99US-0142232P. (GETH) GENENTECH INC 02-JUL-1999;

Dennis MS;

WPI; 2001-123048/13.

Non-naturally occurring peptide ligands which compete for binding human erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy.

Disclosure, Fig 2A, 116pp, English.

This invention relates to non-naturally occurring peptide ligands which bind to the human erbb2 gene product Erbb2 (also known as HER2). Peptides represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples of the Erbb2 binding ligands of the invention. Sequences AAB76421 -

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Gaps

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1; Indels

Mismatches

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Matches 107; Conservative

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AAB76431 represent antibody Fc amino acid sequences used in the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers, diseases of the nervous system musculature and epithelia, e.g. nervous system damage resulting from trauma, surgery, strokes, ischaemia, infection, metabolic disorders, nutritional deficiency or toxic agents. In partitular the synthetic peptide ligands may be used to treat Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy associated with diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a fusion protein, comprising a peptide ligand and an immunoglobulin (Ig) constant region multimerization domain (Ib). The hybrid molecules comprising the peptide ligands and their functional derivatives can be used in the same applications as, a peptide ligand can be used. For example the peptide ligand can bind ErbB2. The peptide ligand may bind to and inhibit the activity associated with a
                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                         2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel fusion polypeptides comprising a peptide ligand domain which functions to target hybrid molecule to target cell, and immunoglobulin constant region multimerization domain.
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Pred. No. 3.6e-50;
1; Mismatches 1;
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98.2%;
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                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                         Sequence 217 AA;
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Score 572; DB 4; Length 217; Pred. No. 3.6e-50;

98.6%;

Query Match Best Local Similarity

Sequence 217 AA;

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This invention relates to an isolated antibody comprising a dimerisation domain and three or more antigen binding sites amino-terminal to the domain. It is extostatic, antilinflammatory, antibacterial, immunosuppressive, antiallergic, an apoptosis inducer, a vaccine and used isorder e.g. cancer in a mammal, for inducing apoptosis of a cancer in gene therapy. Along with a cytotoxic agent, is useful for treating a call, and for killing a B ell or a cell which overexpresses or expresses on ExbB receptor and for treating benign and malignant tumours, inflammatory, angiogenic and immunological disorders. The antibody is also useful for immunodiagnosis of various diseases including cancer, for human therapy in redirected cytotoxicity, and also useful as fibrinolytic agents or vaccine adjuvants, useful as affinity purification agent, in diagnostic assays for detecting the expression of antigen of interest in specific cells, tissue or serum, and useful for blocking an immune response to a foreign antigen. The antigen is internalised faster than a bivalent antibody comprises three or four heavy chain variable domains which are able to combine with three or four heavy chain variable domains polypeptides to form three or four antigen directed against the same antigen. This sequence represents the native sequence human IgG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel engineered antibody useful in therapeutic applications, contains a dimerization domain and three or more antigen binding sites.
                       APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVVHNAKTKP
1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                             Antibody; antigen; immunoglobin; ADCC; CDC; anti-globin response; antibody dependant cell mediated cytotoxicity; complement dependant cytotoxicity; epidermal growth factor receptor; tumour necrosis factor; lymphocyte; terravalent antibody; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiinflammatory; antipsoriatic; dermatological; antiuléer; antiasthmatic; antiarteriosclerotic; antirheumatic; antibacterial; antiarthritic; neuroprotective; immunosuppressive; antianaemic; antiallergic; antidiabetic; gene therapy; human.
                                                                                                      61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                        Native sequence human IgG Fc region sequence humIgG2.
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                                                                                                                                                                                                                              AAG78434 standard; protein; 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2000; 2000US-0195819P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-2001; 2001WO-US008928.
                                                                                                                                                                                                                                                                                                              12-APR-2002 (first entry)
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Human IgG2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the protein sequence of the Fc region of human About 80-1004 of the glycoprotein comprises a glycoprotein having a Fc region. About 80-1004 of the glycoprotein comprises a mature core carbohydrate structure which lacks fucose attached to the Fc region. The glycoprotein preferably comprises an antibody, and the Fc region is preferably a human IgG Fc region is preferably a human IgG Fc region is preferably a human IgG Fc region is preferably a human IgG Fc region is preferably a human IgG. Proporties of the from the following fucose. The antibody may be chimeric, humanised or human and binds a B-cell surface marker, an ErbB receptor, a tumourassociated antigen or an angiogenic factor, CD20, HER2, vascular endothelial growth factor. CD40 or prostate stem cell antigen. The composition is useful for treating cancer, autoimmune disease, an inflammatory disorder or infection in a mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; antibody; IgG2; cytostatic; immunosuppressive; antiinflammatory;
                                                                                                                                                              1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
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                                                                                                                                                                                                                                                                               61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                        Length 217;
                                                                                                                   1; Indels
                                                                     Score 572; DB 5;
Pred. No. 3.6e-50;
1; Mismatches 1;
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                                                                     98.6%;
98.2%;
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Best Local Similarity 98.2
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human IgG2 Fc region
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                        Sequence 217 AA;
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Query Match

98.6%; Score 572; DB 6; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.6e-50;
Matches 107; Conservative 1; Mismatches 1; Indels

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The invention relates to a new composition comprises a variant of a parent polypeptide having at least a portion of a Fc region. The variant mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells more effectively than the parent polypeptide and comprises at least one amino acid modification at position 280 in the accomposition is useful in treating diseases e.g., autoimmune diseases. The present sequence represents the amino acid sequence of a human immunoglobulin G, 1gG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                         2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising a variant of a parent polypeptide having least a portion of a Fe region, useful in treating e.g., autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC; autoimmune disease; human; IgG; immunoglobulin.
                                                                                                                                61 REEQFINSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 572; DB 8; Length 21
Pred. No. 3.6e-50;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 16; 62pp; English
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                                                                                                                                                                                                                                                                                           ADH75378 standard; protein; 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.6%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-2003; 2003US-00370749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2002; 2002US-0358161P
                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.2'
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watkins JD, Allan B;
                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WATK/) WATKINS J D.
(ALLA/) ALLAN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-070755/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2004002587-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG31095
ID ABG3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a fusion protein, which comprises essentially of an immunoglobulin molecule (19 e.g. 1961 Fc or 1962 FC) or tisk fragment and a non-immunoglobulin molecule. The non-immunoglobulin molecule is a protein having the biological activity of glucocerebrosidase (GCR-like protein). Also included are a DNA sequence encoding the fusion protein comprising: (a) a signal/leader sequence. (b) an 19 molecule; or (c) a target protein sequence having the biological activity of GCR. Also crarget protein sequence having the biological activity of GCR. Also included are an expression vector comprising the fusion protein DNA, a host cell for expression the novel fusion protein and comprising the composition comprising the novel fusion protein and at least one pharmaceutical carrier, diluent or excipient. The fusion protein is useful for treating glycolipid storage disorders, specifically Gaucher's disease. Pabry's disease or Tay-Sachs disease. The fusion protein is also useful for the manufacture of a pharmaceutical composition for treating these diseases. The present sequence represents the Human mature 1962 Fc component suitable for inclusion in a fusion protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New fusion proteins with glucocerebrosidase activity, useful for treating glycolipid storage disorders, specifically Gaucher's disease, Fabry's disease or Tay-Sachs disease.
                                                                                                                Human, glucocerebrosidase, GCR, fusion protein, 1gG1, 1gG2, Fc, glycolipid storage disorder, Gaucher's disease, Fabry's disease, Tay-Sachs disease, nephrotropic, antilipemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.6%; Score 572; DB 5; Length 228; 98.2%; Pred. No. 3.8e-50; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 17; 25pp; English.
                                                                             Human mature IgG2 Fc component.
                                                                                                                                                                                                                                                                                                                       27-DEC-2001; 2001WO-EP015328
                                                                                                                                                                                                                                                                                                                                                            18-JAN-2001; 2001EP-00101056
                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gillies S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.6
Best Local Similarity 98.2
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-599719/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 228 AA;
                                                                                                                                                                                                                                       WO200257435-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Schumacher S,
                                 21-OCT-2002
                                                                                                                                                                                                  Homo sapiens.
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> 61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109 ઠે g

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0; Gaps

Search completed: November 17, 2005, 07:04:54 Job time : 91.8333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

November 17, 2005, 06:49:37; Search time 17.9178 Seconds (without alignments) 585.319 Million cell updates/sec Run on:

US-09-674-857-2 580

1 APPVAGPSVFLFPPKFKDTL......CKVSNKGLPSSIEKTISKTK 109 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		df			SUMMAKIES	
Result No.	Score	Ouery Match	Length	DB	ID	Description
-	572	98.6	326	-	G2HU	Id damma-2 chain C
7	536	92.4	327	Н	G4HU	gamma-4
е	529	91.2	377	~	A23511	
4	529	91.2	377	~	A60764	gamma-3
2	526	90.7	234	~	PT0207	
9	524	90.3	255	4	S31866	damma-
7	524		330	٦	Снни	gamma-1
8	524	90.3	374	N	869339	
σ	516	89.0	289	٦	G3HUWI	gamma-
10	457	78.8	328	~	147160	gamma 2
11	457	78.8	328	N	147159	
12	452	77.9	277	~	147162	
13	441	76.0	328	N	147161	gamma 3
14	441	76.0	328	N	147158	
15	429	74.0	470	~	S22080	heavy chain pr
16	425	73.3	308	N	C30554	heavy chain
17	425	73.3	329	Н	G2GP	gamma-2 chain
18	425	73.3	472	~	S31459	
	423	72.9	333	~	PS0018	gamma-
20	418	72.1	323	7	GHRB	
	414		327	7	806611	gamma-2 chain
	410.5	70.8	329	н	G3MSC	gamma-3 chain
	410.5	70.8	398	-1	G3MSM	
	410	70.7	324	Н	GIMS	
25	410	70.7	393	Н	GIMSM	
26	410	70.7	444	7	PC4436	g
27	400	0.69	329	~	S00847	gamma-2c
28	384	66.2	326	~	PS0017	Ig gamma-1 chain C
29	383		335	Н	G2MSAB	

Ig gamma-2b chain	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma heavy cha	Ig epsilon-chain -	Ig epsilon chain C	Ig gamma-1 chain C	Ig heavy chain pre	Ig mu chain C regi
GZMSBM	G2MS11	G2MSA	G2MSAM	S37483	S01321	S40295	PS0019	B30503	A30503	146732	I36948	ЕННО	S14236	S04845	803961
н	Н	н	Ä	N	~	~	N	N	7	~	7	н	7	7	7
405	474	330	399	469	475	446	322	112	88	180	426	428	152	549	457
0.99	0.99	65.2	65.2	65.2	63.6	63.4	59.0	53.4	47.8	43.8	29.9	29.7	29.7	26.9	26.2
383	383	378	378	378	369	368	342	310	277	254	173.5	172.5	172	156	152
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Ig gamma-2 chain C region - human (5/80 peries: Homo sapiens (man) (5/80 peries: Homo sapiens (man) (man) (5/80 peries: Homo sapiens (man) (5/80 peries: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004 (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80 peries) (5/80
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A; Accession: A93906

A; Molecule type: DNA
A; Residues: 1-326 <ELL>
A; Residues: 1-326 <ELL>
A; Cross-references: UNTROT: P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1;
A; Note: Lys-326 is probably removed posttranslationally
A; Note: Lys-326 is probably removed posttranslationally
B; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgC2 heavy chain: genetic, evolutionary, and A; Reference number: A92809; MUID:81007873; PMID:6774012
A; Contents: myeloma protein Til
A; Accession: A92809

A, Molecule type: protein
A, Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193,'D', 195-325 < WAN>
A, Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193,'D', 195-325 < WAN>
A, Rote in the is at or near the complement-binding site
B, Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A, Title: The amino acid sequences of the three heavy chain constant region domains of a A, Title: The amino acid sequences of the three heavy chain constant region domains of A, Reference number: A90752; MUID:80001357; PMID:113060
A, Concents: myeloma protein Zie
A, Reference has protein Zie
A, Residues: 1-24, 'E', 26-57, 'EV', 60-85,132-171, 'ZZZ', 175,'B', 177-193,'D', 195-196,'Q', 198
A, Note: this sequence has since been revised
A, Note: this sequence has since been revised
A, Note: this sequence has since been revised
A, Note: this and the amino acid sequence of residues 381-391 of human immunoglobulin and the amino acid sequence of residues 381-391 of human immunoglobulin and R, Reference number: A93132; MUID:80114419; PMID:118920

A; Accession: A93132

A Molecule type: protein
A. Meaddudes: 238-275 < HOF>
R. Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
Streference number: A94591
A. Contents: amoutation; Zie, revisions to residues 25, 59, 60, and 264-268
A. Note: the revised sequence differs from that shown in having 60-Ala and in the amidat:

R;Milstein, C.; Frangione, B. Biochem. J. 121, 217-225, 1971 A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2. A;Reference number: A90253; MUID:72033500; PMID:4940472 A;Contents: annotation; myeloma protein Sa, disulfide bonds

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Page

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Query Match
Best Local Similarity 94.3%;
Matches 100; Conservative
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Best Local Similarity 92...
Log 98; Conservative
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A;Residues: 1-377 <HUC>
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les 98; Conserv
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB: IGHG3
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C)Sectors (Anon sapiens)
C)Date: 02-Apr.1982 #esquence Tevision 02-Apr.1982 #text_change 09-Jul-2004
C)Sectors: Homos sapiens (mai)
C)Date: 02-Apr.1982 #esquence revision 02-Apr.1982 #text_change 09-Jul-2004
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R;Frangione, B.; Miletein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
C;Genetics:
A;Gene: GDB:119338; OMIM:147110
A;Gene: GDB:119338; OMIM:147110
A;Gene: CDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology <IM2>
F;20-85/Domain: immunoglobulin homology <IM3>
F;31-202/Domain: immunoglobulin homology <IM3>
F;14/Pisulfide bonds: interrchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 326;
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98.6%; Score 572; DB 1; Length 32
Best Local Similarity 98.2%; Pred. No. 6.1e-50;
Matches 107; Conservative 1; Mismatches 1; Indels
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G4HU
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"Gramma-3 chain C region (allotype G3m(b)) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: A2-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999 C;Accession: A23511 Rsquence Laterator, M.P.; Lefranc, M.P.; Lefranc, G. Nucleic Acids Res. 14, 1779-1789, 1986 A;Titles: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: co A;Accession: A23511; MUD:86148507; PMID:3081877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convertance number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
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C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VAGPSVFLFPPKPRDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE
                                                                                                              4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE
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A;Map position: 14q22.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin F;20-85/Domain: immunoglobulin homology <IMM>
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                                                    3; Indels
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92.5%; Pred. No. 1.5e-45;
tive 4; Mismatches 4;
Score 536; DB 1;
Pred. No. 2.6e-46;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.2%; Score 529; DB 2; 92.5%; Pred. No. 1.5e-45; ative 4; Mismatches 4.
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F;20-85/Domain: immunoglobulin homology <IMM>
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A; Molecule type: DNA
A; Residues: 2-330 <HAR>
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$31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: $31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products.
A;Reference number: $31866
A;Accession: $31866
A;Accession: $31866
A;Accession: $1256 FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CA449866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Bscherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
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                                                                                                                                                                                                                                                                      Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: P70207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: P70207, MUID:91287716; PMID:2062315
A;Reference number: P70207, MUID:91287716; PMID:2062315
A;Reference number: P70207, MUID:91287716; PMID:2062315
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
                                21 PPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE
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                                                                                                Length 234;
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1 Similarity 86.8%; Pred. No. 1.7e-45;
99; Conservative 5; Mismatches 4; Indels
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Pred. No. 3.1e-45;
6; Mismatches 4; Indels
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Best Local Similarity 86.0%;
Matches 98; Conservative
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Matches 99; Conserv
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RESULT GHHU

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Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93433; 836861, 833887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Ree. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Accession: A330 < ELL>
A;Residues: 1-330 < ELL>
A;Residues: 1-330 < ELL>
A;Residues: U.J.
A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, b.J.
Submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
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Ajresiques: 2-330 chaxa.

Ajresiques: 2-330 chaxa.

Ajresiques: 2-330 chaxa.

Ajritle: Structure of human immunoglobulin gamma genes: implications for evolution of a Ajreference number: S33887; MUID:83001943; PMID:6811139

Ajreference number: S33887; MUID:83001943; PMID:6811139

Ajresiques: 88-113;238-330 craks

Ajresiques: B8-113;235-330 craks

Ajresiques: B8-113;235-330 craks

Ajresiques: B8-113;235-330 craks

Ajresiques: B8-113;235-330 craks

Ajresiques: B3-113;235-330 craks

Ajresiques: B3-113;2370 craks

Ajresiques: B3-113;2370 craks

Ajresiques: B3-113;2370 craks

Ajresiques: B3-113;2370 craks

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A;Reference number: A91668; MUID:77070269; PMID:826475

A;Accession: B91668

A;Accession: B91668

A;Accession: B91668

A;Molecule type: protein

A;Nolecule type: protein

A;Nole
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A; Residues: 1-96, R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 < SC:
A; Residues: 1-96, R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 < SC:
A; Note: this sequence has the Glm(3) and Glm(non-1) markers
R; Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfit
A; R; Reference number: A90565; MUID:71064027; PMID:4923144
A; Contents: annotation; disulfide bonds
R; Droker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
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A;Molecule type: protein
A;Rolecule type: protein
A;Residues: 136-154, Q',156-165, Q',167-176, Q',178-194, N',196-197, D',199-238, E',240
A;Nesidues: 136-154, Q',156-165, Q',167-176, Q',178-194, N',196-197, D',199-238, E',240
A;Noteingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgGl-Immunglobulins (Myelomprotein Nie)
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A;Residues: 1-96, "R', 98-135 <CUN>
A;Residues: 1-96, "R', 98-135 <CUN>
A;Note: this sequence has the Glm(3) marker, 97-Arg
R;Nutishauser, U.; Cunningham, Bl.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid it A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
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A,Title: Rule of antibody structure. The primary structure of monoclonal Igg1 immunoglob enbromide cleavage products, and the disulfide bridges.
A,Reference number: A91667; MUID:77070267; PMID:1002129
A,Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:1GHG1
A,Cross-references: GDB:120085; OMIM:147100
A;Gene: GDB:1GHG2
A,Cross-references: GDB:120085; OMIM:147100
A;Map position: 1493.33-44932.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c;Complex: An immunoglobulin heterotetramer; immunoglobulin homology cinclessing c;Superfamily: immunoglobulin homology cinclessing c;Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology cinclessing c;Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology cinclessing c;Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology cinclessing c;Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology cinclessing c;Reywords: duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplicatio
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S693139
Ig heavy chain V region precursor - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: S69339; S72664
R; Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Blochem. 229, 34-60, 1995
A; Titls: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A; Reference number: S69339; MUID:95262687; PMID:7744049
A; Accession: S69339
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-374 < KTAA>
A; Cross-references: EMBL:X81695
R; Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A; Reference number: S72664
A; Reference number: S72664
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-140,'C', 142-374 < KTA2>
A; Cross-references: EMBL:X81695
C; Superfamily: immunoglobulin C region; immunoglobulin homology
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Pred. No. 4.2e-45;
6; Mismatches 4;
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Pred. No. 4.9e-45;
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86.0%;
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Best Local Similarity 86.0%;
Matches 98; Conservative
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nes 98; Conservative
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RESULT

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A,Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-A,Reference number: A90442, MUID:81021548; PMID:6774747
A,Contents: heavy chain disease protein Wis
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A, Residues: 1-289 FRA>
A, Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A, Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co
A, Note: the sequence of residues 42-76 was taken from the reference that follows
R, Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
A, Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A, Reference number: A92219; MUID: 77118561; PMID: 402263
A, Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 12-97 < MIC> A; Rosidues: the hinge region in gamma-3 chains is about four times as long as in other gammalique segment (12-28)
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A,Molecule type: protein

A,Residues: 59-125, EB., 128-226, 228-289 <WOL>
A,Residues: 59-125, EB., 128-226, 228-289 <WOL>
A,Residues: 59-125, EB., 128-226, 228-289 <WOL>
A,Rote: this protein lacks most of the V region, all of the CHI region, and part of the R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L., Proc. NaLL. Acad. Sci. U. S.A. 79, 2360-3264, 1982

A;Alticle: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion A;Reference number: A93915, MUID:82247835; PMID:6808505

A;Acontents heavy chain disease protein Omm

A;Accession: A93915

A;Molecule type: mRNA
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A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
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                                                                                                                                              #text_change 16-Jul-1999
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Iggamma-3 heavy chain disease proteins - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence revision 23-Oct-1981 #text_cha
C;Accession: A90219; A92219; A90198; A93915; A02149
R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, B.C.
Biochemistry 19, 4304-4308, 1980
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7; Mismatches 4;
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Ig gamma 2b chain constant region - pig (fragment)
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76.0%;
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Best Local Similarity 77.9%
Matches 81, Conservative
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R;Kacskovics, I: Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147158, MUID:95015845; PMID:7930579
A;Reference number: 147159
A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-328 «KAC>
A;Residues: 1-328 «KAC>
A;Cessereferences: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Kacsesvious, I.; Suu, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: I47158; MUID:95015845; PMID:7930579
                                                                                                                                 of
           C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000 C; Accession: 147160 R; Kacskovics, I.; Sut, J.; Butler, J.E.

R; Kacskovics, I.; Sut, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences cA; Reference number: 147158; MUID:95015845; PMID:7930579
A; Reference number: 147158; MUID:95015845; PMID:7930579
A; Reference number: 147158; MUID:95015845; PMID:7930579
A; Residues: 1-328 cKAC>
A; Residues: 1-328 cKAC>
A; Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: immunoglobulin C region; immunoglobulin homology
F; 133-202/Domain: immunoglobulin homology <IMM>
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Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb.1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Best Local Similarity 78.8%; Pred. No. 2.3e-38;
Matches 82; Conservative 13; Mismatches 9;
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Best Local Similarity
Matches 82; Conserv
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Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
R;Racskovics, I: Sun, J:, Butler, J.E.
J: Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A;Reference number: I47158; MUID:95015845; PMID:7930579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Accession: I47161
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47161
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPBVQFNWYVDGVEVHNAKTKPREEQF
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C;Genetics:
A;Gene: IgG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC.
A;Residues: 1-328 <KAC.
A;Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 NSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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Pred. No. 9.2e-37;
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A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
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Syzugo

NyAlterrate names: Ig gamma-1 chain C region (clone 8.10)

C;Specises: Bos primigenius taurus (cattle)

C;Specises: Bos primigenius taurus (cattle)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S22080; S06610; Ā31303

R;Sanders, P.G.

Submitted to the EMBL Data Library, November 1991

A;Rccession: S22080

A;Scatus: preliminary

A;Molecule type: mRNA

A;Residues: 1-470 & SAN>

A;Ccession: CA,: Beale, D.

A;Cression: S2080

A;Cress-references: EMBL: K52916; NID:9439; PIDN:CAA44699.1; PID:9440

R;Symons. D.B.A.; Clarkson, C.A.; Beale, D.

Mol: Immunol. 26, 841-850, 1989

A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma

A;Reference number: S06610; MUID:90097956; PMID:2513487

A;Accession: S06610

A;Molecule type: DNA

A;Residues: 142-470 & SYM>

A;Accession: S06610

A;Molecule type: DNA

A;Residues: 119 CH samma-1

A;Antcons: 98/1; 111/1; 221/1

A;Antcons: 98/1; 111/1; 221/1

A;Antcons: 98/1; 111/1; 221/1

A;Antrons: 98/1; 111/1; 221/1
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                                                                                                               Length 328;
C,Superfamily: immunoglobulin C region; immunoglobulin homology F;133-202/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                              64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                   174 QFNSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISK 217
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                                                                                                                                                                                  11; Indels
                                                                                                        Query Match 76.0%; Score 441; DB 2; Best Local Similarity 77.9%; Pred. No. 9.2e-37; Matches 81; Conservative 12; Mismatches 11;
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MEDLINE=83001943; PubMed=6811139; DOI=10.1016/0092-8674(82)90183-0;
Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
Cell 29:671-679(1982).
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SEQUENCE OF 238-275 (ZIE).
MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;
                              homo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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P20761
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Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
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Last annotation update)
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MEDLINE-81007873; PubMed-6774012;
Wang A.-C., Tung E., Rudenberg H.H.;
"The primary structure of a human 1gG2 heavy
evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
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MEDLINE=6423592; PubMed=6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments heavy chain genes and the linkage of the genes.";
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SEQUENCE OF 99-177 AND 310-326 FROM N.A.
GC1_MOUSE
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 NCBI_TaxID=9606;
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GC2_HUMAN
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S -> A (in myeloma proteins TiL and ZIB).
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C -> S (in Ref. 3).
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Milstein C., Frangione B.;
"Disulphide bridges of the heavy chain of human immunoglobulin G2.";
Biochem. J. 121:217-225(1971).
                                                                                                                                                                                                              MEDLINE-95255298; PubMed-7737190;
Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri
"Characterization of the two unique human anti-flavin monoclonal
    Hofmann T., Parr D.M.;
"A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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MIM, 147110.
GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0006525; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR003597; Ig c1.
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PROSITE; PS50835; IG LIKE; 3.
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DB 1; Length 326;

98.6%; Score 572;

Query Match

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                                                                                       111 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVAGESVFLEPPKENDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                              1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Human esophagus tumor;

THE German Human cDNA Consortium;

Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Fobo G., Han M., Wiemann S.;

Submitted (ANG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640623; CAR45777.1;

HSSP; P01861; 1ADO.
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                                                                                                                                                                        61 REEQFINSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 572; DB 2; Length 417;
Pred. No. 7.3e-49;
1; Mismatches 1; Indels
  Indels
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                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686104196 (Fragment).
  1;
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.-like.
InterPro; IPR003507; Ig_cl.
InterPro; IPR003596; Ig_w.
InterPro; IPR003596; Ig_w.
SMART; SM00409; IG; 2.
SWART; SM00400; IG; 3.
SWART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MKC; UNKNOWN_2.
Hypothetical protein.
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249 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGMEVHNAKTKP 308
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In German cDMA consortium;

Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,

Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,

Changer A., Fobo G., Han M., Wiemann S.;

Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; CR749861; CAH18705.1; -..

R InterPro; IPR003599; Ig.,

InterPro; IPR003599; Ig.,

InterPro; IPR003597; Ig.,

InterPro; IPR003506; Ig.W.

R InterPro; IPR003506; Ig.W.

R InterPro; IPR003506; Ig.W.

R Ffam; PF00647; ig; 4.

R Ffam; PF00647; ig; 4.

R SWART; SM00409; IG.2

R SWART; SM00409; IG.2

R SWART; SM00406; IG.Y 1.

R PROSITE; PS00290; IG.MHC; UNKNOWN_2.

Hypothetical protein.

T NON_TER
                                                        TISSUE-Human rectum tumor;

THe German Human cDNA Consortium;

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (ANG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX440874; CAE45931.1;

HSSP; P01861; 1ADQ.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             493 AA; 54117 MW; AIE4FSED3FA8AB40 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686E23209 (Fragment)
Name=DKFZp686E23209,
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 569; DB 2;
Pred. No. 1.6e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_WHC.
Pfam; PF00564; C1-set; 3.
SWART; SW00409; IG; 2.
SWART; SW00409; IG; 1.
PR051TE; PS00359; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 98.1%;
Best Local Similarity 97.2%;
Matches 106; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.18;
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TISSUE=Rectum tumor;
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25-OCT-2004
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**Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

**A Lausner R.D., Colling F.S., Wagner L., Sheamen C.M., Schuler G.D.,

**A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

**A Popkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

**Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

**A Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

**A Robert S., McKwam P.J., McKernan K.J., Maruson R.D., Mullahy S.J.,

**Bosak S.A., McKwam P.J., McKernan K.J., Maruson R.D., Mullahy S.J.,

**A Richards S., Worley K.C., Hale S., Garrenan R., Gap L.J., Hulyk S.W.,

**A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**A Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Multing M. Mara M.A., Young A.C., Shewrokenko Y., Bouffard G.G.,

**A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

**A Nones S.J., Marra M.A.,

**Jones S.J., Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 8.2e-49;
1; Mismatches 1
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PROSITE; PS00230; IG_MHC; UNKNOWN_2.
HYPOTHETICAL DIVETEIN
SEQUENCE 465 AA; 51325 WW, FDDB95
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; C1-set; 3.
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98.2%;
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Best Local Similarity 98.28
Matches 107; Conservative
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SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
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NCBI_TaxID=9606;
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01-JUN-2002
01-JUN-2002
01-MAR-2004
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                               64 OFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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                  Indels
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SEQUENCE 476 AA; 52420 MW; 0D3D1FFE5853958F CRC64;
                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686M24218.
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95.3%; Pred. No. 1.7e-45;
iive 2; Mismatches 3;
                    3;
 96.3%; Pred. No. 7e-48; ive 1; Mismatches
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21-JUL-1986 (Rel. 01, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
1g gamma-4 chain C region.
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Best Local Similarity 96.3
Matches 105; Conservative
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Matches 101; Conservative
                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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P01861;
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                                                                                                                                                                                                                  Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the
constant region of a gamma 4 chain.";
Blochem. J. 117:33-47(1970).
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              MEDLINE-83157104; PubMed-6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
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Interchain (with a heavy chain)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 OFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 536; DB 1; Length 32
Pred. No. 2.2e-45;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35940 MW; 3EDBD811EF208E7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A90933; G4HU.
PDB; 1ADQ; X-ray; A=118-323.
Genew; HGNC:5528; IGHG4.
MIM; 147130; -.
GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0009823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR00710597; Ig-d1.
InterPro; IPR007105; Ig-d1.
InterPro; IPR007106; Ig-MHC.
PMART; SMO0407; IG: J.
PROSITE; PS06835; IG_LIKE; 3.
PROSITE; PS06290; IG-MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CH1.
Hinge.
CH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; K01316; AAB59394.1; ALT_INIT.
                                                                                                                                                               SEQUENCE OF 1-30 AND 81-326.
MEDLINE=70207560; PubMed=4192699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.4%;
94.3%;
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(TrEMBLrel. 21, I
(TrEMBLrel. 26, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3D-structure, Direct p
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
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                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 473;
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94.3%; Pred. No. 3.4e-45;
...marches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025985; AAH25985.1; -.
HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00196; COPPER BLUE; UNKNOWN_1.
PROSITE; PS000290; IG LIKE; 4.
PROSITE; PS000290; IG MAC, UNKNOWN 3.
SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
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Last annotation update)
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; C1-8et; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLJ00385 protein (Fragment)
Name=FLJ00385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences."
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IGHG4 protein.
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                 NCBI_TaxID=9606;
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1D 08NF
AC 08NF
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
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Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Villalon D.K., Munny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Mhiting M., I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
March D. Marra M.A.,
Understion and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                 Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO90464; BAC03445.1; -.
PIR, A45874; A45874.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF07654; Cl-set; 3.
SMART; SW00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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01-OCT-2002 (TrEMBLrel. 22,
01-MR-2004 (TrEMBLrel. 26,
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Best Local Similarity
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GC1_HUMAN
P01857;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                  4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODI019YF20 of Placenta of Homo sapiens (human) (Fragment).
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                                                                                                                                                                                                                                                                                                             Length 521;
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Best Local Similarity 92.5%; Pred. No. 1.2e-44;
Matches 98; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                         4; Indels
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TISSUB=placenta;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248278; CAD62606.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                    57156 MW; 2AC7D22E72D6CAA2 CRC64;
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                                                                                                                                                                                                                                                                                                           Query Match 91.7%; Score 532; DB 2; Best Local Similarity 93.4%; Pred. No. 9.5e-45; Matches 99; Conservative 3; Mismatches 4
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Interpro; IPR003597; Ig_c1.
Interpro; IPR003506; Ig_MHC.
Incerpro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; 3.
SMART; SM0406; IGv.
PROSITE; PS08283; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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  BC033178; AAH33178.1;
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                    PIR; A60764; A60764.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                             Hypothetical protein
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TISSUE=Placenta;
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TISSUE=Human rectum tumor;

TISSUE=Human rectum tumor;

TISSUE=Human rectum tumor;

The German Human cDNA Consortium;

A Poutska A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,

A Boust A., Neil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

Submitted (AuG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, BK640-24; CAE45841.1; -.

BKNSP; P01861; 1ADQ.

InterPro; IPR001059; HTHARAC.

InterPro; IPR001059; Ig.

InterPro; IPR001597; Ig.

InterPro; IPR001597; Ig.

InterPro; IPR001597; Ig.

InterPro; IPR001596; Ig.

InterPro; IPR001596; Ig.

InterPro; IPR00169; IG; 3.

SNART; SM00407; IG.1; 3.

SNART; SM00407; IG.1; 3.

SNART; SM00407; HTH ARAC FAMILY_1; UNKNOWN_1.

PROSITE; PS0001; HTH ARAC FAMILY_1; UNKNOWN_2.

HUMCHARIE; PROSISE; IG. MHC; UNKNOWN_2.
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MEDLINB=82274238; PubMed=6287432;
Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin C gammal gene.";
"Vocleic Acids Res. 10:4071-4079(1982).
                             06-0030, 05-004 (TERMELrel. 27, Created) 05-004 (TERMELrel. 27, Last sequence update) 05-004 (TERMELrel. 27, Last sequence update) 05-004 (TERMELrel. 27, Last annotation update) Mame-DKFZp686115212. Mame-DKFZp686115212. Howo sapiens (Human). Eukaryota, Metazoa; Ghordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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92.5%; Pred. No. 1.9e-44;
ive 4; Mismatches 4; Indels
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SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;
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518 AA
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21-JUL-1986 (Rel. 01, Last seq
25-OCT-2004 (Rel. 45, Last ann
Ig gamma-1 chain C region.
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AAC82527.1; ALT INIT
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| 1054; X-ray; H=1-101.
| 1086; X-ray; H=1-101.
| 1084; X-ray; A/B=106-329.
| 1672; X-ray; A/B=106-329.
| 1672; X-ray; A=121-329.
| 1172; X-ray; H/K=1-330.
| 1173; X-ray; A/B=107-330.
| 1118; X-ray; A/B=107-330.
| 1118; X-ray; A/B=107-330.
| 1118; X-ray; A/B=107-330.
| 1063; X-ray; A/B=107-330.
| 1063; X-ray; A/B=107-330.
| 1063; X-ray; A/B=109-330.
                                                                                                                           ; X-ray; B/H=1-101,
; X-ray; H=1-101,
; X-ray; H=1-101.
                              EMBL; J00228; AAC82527.1; PDR; A9343; GHHU. PDB; LAJ7, X-ray; B/H=1.103 PDB; LD5B; X-ray; B/H=1.101 PDB; LD5B; X-ray; B/H=1.101 PDB; LD5I; X-ray; H=1.101 PDB; LDX; X-ray; H=1.101 PDB; LDX; X-ray; H=1.101 PDB; LR4K; X-ray; A/B=1.06 PDB; LRC1; X-ray; A/B=1.06 PDB; LRC2; X-ray; A/B=1.07 PDB; LRC2; X-ray; A/B=1.07 PDB; LIX; X-ray; A/B=1.07 PDB; LL6X; X-ray; X-ray; A/B=1.07 PDB; LL6X; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; 
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Blochemistry 20:2261-2270(1981).
-! MISCELLANBOUS: Nie has the GIM(17) allotypic marker, 97-K, and the GIM(1) markers and the GIM (100-1) markers.
-! MISCELLANBOUS: Nie also differs in the amidation states of 35, 116, 198, 269 and 272.
-! MISCELLANBOUS: EU also differs in the amidation states of residues 155, 166, 177, 195, 198, 269, and 272 and in the order of residues 268-272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE (MYELOMA PROTEIN NIE).
MEDLINE=77070269; PubMed=826475;
Ponsting1 H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a monoclonal 1gG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
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                                                                                                                           "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments HI-H4."; Biochemistry 9:3161-3170(1970).
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MEDLINE-81289131; PubMed=6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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"Rule of antibody structure. The primary structure of a monoclonal
IRule of antibody structure. The primary structure of a monoclonal
IRule of antibody structure. The primary structure of a monoclonal
characterization of the protein, The L- and H-chains, the cyanogen
bromide cleavage products, and the disulfide bridges.";
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                                                                                                                                                                                                                                                                           MEDLINE-71064025; Pubmed-5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
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BEDLINE-17064024; PubMed=5489771;
Cunningham B.A., Rutiahauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M.;
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MEDLINE-81208100; PubMed-7236608;
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MEDLINE=71064027; Pubmed=4923144;
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MEDLINE=77070267; PubMed=1002129;
                                                                                                                                                                                                                                                       SEQUENCE OF 136-329 (EU)
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N-linked (GlcNAC. .).
K -> K (in GlM(3) marker).
/FIId=VAR 00388.
D -> E (in GlM(non-1) marker).
/FIId=VAR 003887.
L -> M (in GlM(non-1) marker).
/FIId=VAR_003888.
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GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0003823; F:antigen binding; TAS.
InterPro; IPRO03100; Ig-like.
InterPro; IPRO03006; Ig_MHC.
PERM; PRO047; Ig. 3.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50836; IG_MHC, 2.
3D-structure; Direct protein sequencing; Glycoprotein; Immunoglobulin C region; Immunoglobulin Gomain.
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TISSUE=Primary B-Cells,

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.D., Peingold E.A., Grouse L.H., Derge J.G.,

Alusoner R.D., Collins P.S., Wagner L., Schamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina R., Farmer A.A., Rubin G.M., Hong L.,

As brownstein M.J., Usdain T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Villalon D.K., Wuzny D.M., Sodersien E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Minting M., Madan A., Young A.C., Schwechenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rymyninski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Jones S.J., Marra M.A.;
                                         PP-----VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PP-----VAGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                188 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH73766.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.-I.
InterPro; IPR003006; Ig WHC.
InterPro; IPR003596; Ig WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.3%; Score 524; DB 2;
86.0%; Pred. No. 5.3e-44;
ative 6; Mismatches 4;
                                                                                                                                                                                                                                                               465 AA
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SMART; SM00407; IG: 13.
SMART; SM00406; IG: 13.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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Pfam; PF00047; ig; 4.
                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. Homo sapiens (Human).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 3.8e-44;
6; Mismatches 4; Indels
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Zhu N.S., Chen Y.Y.,
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sentotation update)
Hepatitis B virus receptor binding protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36106 MW; 3770EE106C2FA33D CRC64;
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Pred. No. 3.6e-44;
6; Mismatches 4;
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330 AA;
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56 AKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum DB
                                                                                            OM protein
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                                                                                                                                             Run on:
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No.
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-	28 30 31	572 572 572 572	98.6	530 530 530	W 4 4 TO	US-09 US-08 US-09 PCT-U	US-09-409-006A- US-08-484-681-4 US-09-766-995-4 PCT-US93-07422-	168 168 168 168 168 168 168 168 168 168	Sequence Sequence Sequence Sequence	4444	Appli Appli Appli Appli	
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RESULT US-09-	1 968-3	62A-18			00	46968367) 211	á					
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******		CANT: Sun, Bill CANT: Sun, Cecil; OF INVENTION: FC	HIONE	Sun, Bill Sun, Cecily R NVENTION: Fc fue	ion	prot	of	human granulocyte	syte colony-stimulaing	r-stim	ulaing factor	ior
	TITLE OF INVENTION: increased biological. FILE REFERENCE: 0380N2001 CURRENT APPLICATION NUMBER: US/09/968,362ACURRENT FILING DATE: 2001-10-01 NUMBER OF SEQ. ID NOS: 28	INVEN ERENCE APPLIC FILING	TION S: 038 PTION I DATE	ON: incre 03SUN2001 1ON NUMBER 0ATE: 2001	: u	increased biologi(12001 UMBER: US/09/968; 2001-10-01 28	biological a /09/968,362A 01	ctivities				
	SOFTWARE: Pat EQ ID NO 18 LENGTH: 448 TYPE: PRT	KE: Pate VO 18 I: 448 PRT	Patentin 8 48	version	m.	ц.						
0-SD	ORGANI PEATUR OTHER OTHER 9-968-	SM: Artific: E: INFORMATION INFORMATION: 362A-18	TION	ial Sequence : hG-CSF-L-vFc : 2A)	enc		gamma2 with	n a 30-amino	acid	ler pe	leader peptide (Figure	ure
ŌάΣ	Query Match Best Local Matches 10	' Match Local Similarity es 108; Conser	larit Conse	99.5% larity 99.1% Conservative	₩.₩.	Sco Pre 1,	re 577; DB d. No. 2.7e- Mismatches	OB 4; Length 4 7e-59; s 0; Indels	448; 1s 0;	Gaps	;0	
<i>&</i> 8	7	1 APF 233 APF	VAGPS	SVELFPPK SVFLFPPK	8-8	TLMIS!	TPEVTCVV	APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 	WYVDGVEVHN	AKTKP	. 292	
, d	- 70	61 REE 293 REE	OFNST 	FRWSVI FRWSVI	\$ <u>_</u> \$	HODWLA HODWLA HODWLA	IGKEYKCKV IIIIIIIII	REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 	ISKTK 109 SKTK 341			
RESULT US-08- ; Sequ	SULT 2 :-08-444-644-30 Sequence 30, Application US/0844644 Patent No. 6015555	44-30 30, AE . 6015	plice 555	ation US	/08	44464	_					
	GENERAL INFORMATION: APPLICANT: Friden, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:	INFORMATION: CANT: Friden, OF INVENTION: OF INVENTION: OF INVENTION:	ATION: Friden, ENTION: FENTION: GUTION:	A: DN: Phil DN: TRA DN: ANT DN: CON	lip NSF TBO	hillip M. TRANSFERRIN ANTIBODY-NEU CONJUGATES 46	Phillip M. TRANSFERIN RECEPTOR SPECIFIC ANTIBODY-NEUROPHARMACEUTICAL CONJUGATES	SPECIFIC	DIAGNOSTIC	AGENT		
	CORRESPON ADDRESS STREET:	RRESPONDEN ADDRESSEE: STREET: T	ICE AI Han wo Mi	CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Broo STREET: Two Militia Drive	Bro	*	Smith & Re	Reynolds, P.C.				

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAMER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-05P-1990
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-05P-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-05P-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-05P-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
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REFERENCE/DOCKET NUMBER: 34,480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.2<sup>3</sup>
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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US-09-483-588-5
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US-08-232-246A-30
is Sequence 30, Application US/08232246A
is Sequence 30, Application US/08232246A
is Partent No. 6322550B
is GENERAL INFORMATION:
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: APPLICABLES
ITILE OF INVENTION: CONJUGATES
ITILE OF INVENTION: CONJUGATES
INVERTION: ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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Pred. No. 1.7e-59;
1; Mismatches 1; Indels
                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: 34,480
TELECOMMUNICATION INPORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ 10 NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                    PELLING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATE:
APPLICATION DATE: 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATE: 07-JUL-1994
PRIOR APPLICATION DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: O7-SEP-1990
PRIOR APPLICATION NUMBER: O7-SEP-1990
PRIOR DATE: 07-SEP-1990
PRIOR DATE: 07-SEP-1990
ATTONEY, AGENT INFORMATION:
                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i: 109 amino acids
amino acid
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Best Local Similarity 98.2
Matches 107; Conservative
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FRAGMENT TYPE: internal
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
        Lexington
                                                         USA
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                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09483588
Patent No. 6737056
GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: Polypeptide Variants with Altered Effector Function
FILE REPERBENCE: P172681
CURRENT APPLICATION NUMBER: US/09/483,588
CURRENT FILING DATE: 2000-01-14
FEARLIER FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
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                                                                    Gaps
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   Length 109;
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                                                             1; Indels
Query Match

98.6%; Score 572; DB 3;
Best Local Similarity 98.2%; Pred. No. 1.7e-59;
Matches 107; Conservative 1; Mismatches 1;
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Query Match
Best Local Similarity 98.2
Matches 107; Conservative
TELEX: 422523 COOP UI INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 432 amino acid
                                                                                                                                                                                                            ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-08-477-460B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                          Sequence 27, Application US/09968362A

Sequence 27, Application US/09968362A

Patent No. 679743

GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Bill
APPLICANT: Sun, Cecily R

TITLE OF INVENTION: For fusion proteins of human granulocyte colony-stimulaing factor TITLE OF INVENTION: increased biological activities
FILE REFERENCE: 03SUN2001

CURRENT APPLICATION NUMBER: US/09/968,362A

CURRENT FILING DATE: 2001-10-01

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 27

LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
APPLICANT: Progenics Pharmaceuticals, Inc.
APPLICANT: Progenics Progenics Progenics Progenics NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMWA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
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62 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human 1gG2 Fc with native hinge, CH2 and CH3 domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 572; DB 4; Length 228;
Pred. No. 4.4e-59;
1; Mismatches 1; Indels
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION:
TELEPHONE: (212) 977-9550
TELEFPAX: (212) 977-9809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10.12
ZIP: 10.12
ZIP: 10.12
ZIP: 10.12
ZIP: 10.12
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION NUMBER: US/08/477,460B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 07/927,931
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-ANG-1995
ATTORNEY AGENT INFORMATION:
NUMBER: 07-ANG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08477460B Patent No. 6034223
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98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 107; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                     US-09-968-362A-27
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APPLICANT: Allaway, Graham P.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: No. 608478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
TITLE OF INVENTION: Immunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
CURRENT APPLICATION NUMBER: US/08/379,516
CURRENT PILING DATE: 1996-06-10
EARLIER PILING DATE: 1996-06-10
EARLIER PILING DATE: 1992-08-07
NUMBER: O7/927,931
EARLIER PILING DATE: 1992-08-07
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: PLENTING DATE: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                              1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
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                                                                                                                                                                                                                         DB 3; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 572; DB 3;
Pred. No. 1e-58;
1; Mismatches 1
                                                                                                                                                                                                                         Score 572; DB 3;
Pred. No. 1e-58;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08379516
Patent No. 6083478
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LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                       Query Match 98.6%;
Best Local Similarity 98.2%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.6%;
98.2%;
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
                                                                                                                                                                                                                                                                                 37690-II-A
                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,372A
                                                                                            CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,227
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-I:
TELEPHONE: (212) 278-0400
TELEFRAX: (212) 391-0525
     SOFTWARE: Patentin Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 98.2%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-08-485-372A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 30 Rockes
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10112
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US-09-409-006A-2
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                                                                                                       COMPUTER: USAN

ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,916
FILING DATE:
CLASSIFICATION NUMBER: US/09/329,916
FILING DATE:
APPLICATION NUMBER: US/09/329,916
FILING DATE: US O7-JUN-1995
APPLICATION NUMBER: US O7/927,931
FILING DATE: US O7-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELEPHONE: (212) 977-9850
TELEPHONE: (212) 977-9850
TELEPHONE: (212) 977-9850
TELEPHONE: (212) 977-9850
TELEPHONE: (212) 977-9850
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TELEPHONE: (212) 977-9850
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APPLICANT: Maddon, Paul J.
TITLE OF INTURNITION: CD4-GAMMA2 CD4-IgG2 CHIMERAS NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 572; DB 3;
Pred. No. 1e-58;
1; Mismatches
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STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08485372A Patent No. 6187748 GENERAL INFORMATION:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.2%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: homo sapien ; CELL TYPE: lymphocyte US-09-329-916-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                 New York
: New York
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS: unl
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STATE: New York
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                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-485-372A-2
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Sequence 2, Application US/09409006A
Patent No. 6342586
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-1gG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: Cooper & Dunham
STREFT: 30 Rockefeller Plaza
                                                                                                                                                                 217 APPVAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
                                                                                                                               1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVOFNWYVDGVEVHNAKTKP
                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                   277 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 325
Score 572; DB 3; Length 432;
Pred. No. 1e-58;
1; Mismatches 1; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                           Query Match 98.6%; Score 572; DB 3; Length 432; Best Local Similarity 98.2%; Pred. No. 1e-58; Matches 107; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08484681
Fatent No. 6451313
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UGA
ZIP: 10036
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION UNMBER: US/08/484,681
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-B
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEFAX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
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TYPE: amino acid
STRANDEDNESS: unknown
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                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                          homo sapien
                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                               CELL TYPE: lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-08-484-681-2
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                           TYPE: amino & STRANDEDNESS:
                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                    US-09-409-006A-2
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Sequence 2, Application US/09766995

Sequence 2, Application US/09766995

Patent No. 6737267

GRNERAL INFORMATION:

GRNERAL INFORMATION:

GRNERAL INFORMATION:

TITLE OF INVENTION: NON-PEPTINYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJ

TITLE OF INVENTION: AND USES THEREOF

FILE REPERENCE: 20404/1215-CG4/DFW/SHS

CURRENT APPLICATION NUMBER: US/09/766,995

CURRENT FILING DATE: 2001-01-22

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PATENTIN Version 3.0

SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Progenice Pharmaceuticals, Inc.
APPLICANT: Progenice Pharmaceuticals, Inc.
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                         217 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 APPVAGPSVFLFPPFKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 276
                                                                                                         1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
Score 572; DB 4; Length 432;
Pred. No. 1e-58;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.6%; Score 572; DB 4; Length 432; Best Local Similarity 98.2%; Pred. No. 1e-58; Matches 107; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
     Query Match 98.6%;
Best Local Similarity 98.2%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: homo sapians
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
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US-09-766-995-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 572; DB 5; Length 432;
Pred. No. 1e-58;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INCORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSEN, MARK J.
APPLICANT: MUSULER, BILLEN E.
APPLICANT: MUSULER, BILLEN E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REPRENCE: ABX-PBL
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
FRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SOUTHWARE: PARCHIN UNC: 147
SOUTHWARE: PARCHIN UNC: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 572; DB 4; Length 451;
Pred. No. 1.1e-58;
1; Mismatches 1; Indels
                NAME: White, John P.

REGIGTRATION NUMBER: 28 678
REGIGTRATION NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-950
TELERA: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
NOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 70, Application US/09472087; Patent No. 6682736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.6%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.2%;
Matches 107; Conservative
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 98.2
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: homo sapien
CELL TYPE: lymphocyte
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US-09-472-087-70
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RESULT 15

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; Betent No. 6682736
; GENERAL INPORMATION:
   APPLICANT: HANSON, DOUGLAS C.
   APPLICANT: HANKE, DELEN E.
   APPLICANT: HANKE, JEFFREY H.
   APPLICANT: GILMAN, STEVEN C.
   APPLICANT: GILMAN, STEVEN C.
   APPLICANT: GILMAN, STEVEN C.
   APPLICANT: CONVALAN, JOSE R.
   APPLICANT: CONVALAN, JOSE R.
   TILLE REFERENCE: ABX-PF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 572; DB 4;
Pred. No. 1.1e-58;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.2%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1
LENGTH: 463
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November 17, 2005, 07:05:08; Search time 83.6164 Seconds (without alignments) 545.427 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB_pep:*
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22: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1867879 seqs, 418409474 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                       - protein search, using sw model
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seq length: 200000000
                                                                                                                                                                                                                                                                                                                   US-09-674-857-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Maximum DB E
                                                                                                                          OM protein
                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	;			Appl	Appl	Appl	Appl	Appl	Appl	Appli	ppli	Appli
	.	16,	18,	18,	18,	18,	18,	18,	18,	7	, A	'n
	Description	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 2,	Sequence 3, Appli	Sequence 3,
		US-10-745-775-16	09-932-812-18	10-761-593A-18	11-016-518A-18	11-017-185-18	19-968-362-18	10-800-497-18	10-800-449-18	US-10-959-318-2	9-813-341-3	US-10-277-370-3
ó	01	US-1	ns-(US-1	US-1	US-1	ns-(US-1	US-1	US-1	SO-SO	US-1
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	Length	447	436	436	436	436	448	448	448	109	217	217
	% Query core Match Length DB ID	100.0	99.5	99.5	99.5	99.5	99.5	99.5	99.5	98.6	98.6	98.6
	Score	580	577	577	577	577	577	577	577	572	572	572
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Gaps

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Indels

1 APPVAGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP

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Sequence 14, Appl Sequence 15, Appl Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 28, Appl Sequence 28, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 21, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 27, Appl Sequence 37, Appl Sequence 37, Appl Sequence 27, Appl Sequence 37,	a) O
14 US-10-196-394-74 15 US-10-370-749-16 16 US-10-77-863-5 17 US-10-982-647-5 18 US-10-982-470-5 19 US-10-982-470-5 19 US-10-982-470-5 10 US-10-982-470-5 10 US-10-980-449-27 20 US-11-016-518A-27 20 US-11-016-518A-27 20 US-11-016-518A-27 21 US-10-981-0775-449-27 22 US-10-983-591-28 23 US-10-928-305-8 24 US-10-928-305-8 25 US-10-928-305-8 26 US-10-928-305-8 27 US-10-928-305-8 28 US-10-928-305-8 29 US-10-928-305-8 20 US-11-01-980-6 20 US-11-01-980-6 20 US-11-026-998-23 20 US-11-026-998-23 20 US-11-026-998-23 21-02-981-026-998-23 22 US-11-026-998-23 23 US-10-981-026-998-23 24 US-10-775-448-23 25 US-11-026-998-23 26 US-11-026-998-23 27 US-11-026-998-23 28 US-09-766-995-2	20 US-11-034-655-9
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	98.6
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	572
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ALIGNMENTS

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Length 447;
                                                                      SERVEAL INTOCALATION.

STATE OF INVENTION.

TITLE OF INVENTION: SAME

TITLE OF INVENTION: SAME

FILE REPERENCE: 514712001400

CURRENT APPLICATION NUMBER: US/10/745,775

CURRENT FILING DATE: 2003-12-24

PRIOR FILING DATE: 2003-12-24

PRIOR PILING DATE: 2003-12-24

PRIOR PRIOR PLICATION NUMBER: US 60/43,522

PRIOR PRICE 2003-12-8

PRIOR PRICE 2003-10-08

PRIOR FILING DATE: 2003-10-08

PRIOR FILING DATE: 2003-10-08

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FABLESQ for Windows Version 4.0

SEQ ID NO 16.

LENGTH: 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic Construct US-10-745-775-16
Sequence 16, Application US/10745775 Publication No. US20040237124A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
APPLICANT: Sun, Bill N
APPLICANT: Sun, Cccily R
TITLE OF INVENTION: activities
TITLE OF INVENTION: activities
FILE REFERENCE: 0.25UN2001D2
CURRENT APPLICATION NUMBER: US/11/017,185
CURRENT APPLICATION NUMBER: US/11/017,185
RIOR APPLICATION NUMBER: US 09/932,812
RROR FILING DATE: 2004-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2 ) OTHER INFORMATION: A) US-11-017-185-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure OTHER INFORMATION: 2A)
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
APPLICANT: Sun, Ceily R
APPLICANT: Sun, Ceily R
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased TITLE OF INVENTION: biological activities
FILE REPERENCE: 02cut00401
CURRENT APPLICATION NUMBER: US/11/016,518A
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US 09/932,812
PRIOR APPLICATION NUMBER: US 09/932,812
PRIOR APPLICATION NUMBER: US 09/932,812
PRIOR APPLICATION NUMBER: US 09/932,812
PRIOR APPLICATION NUMBER: US 09/932,812
PRIOR PRIOR DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
                                      1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
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                                                                                                              61 REEQFINSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                             281 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPASIEKTISKTK 329
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Pred. No. 2.4e-48;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            Sequence 18, Application US/11016518A Publication No. US20050124045A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-017-185-18; Sequence 18, Application US/11017185; Publication No. US20050142642A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORCANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.1%;
Matches 108; Conservative
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| Publication No. US20040175824A1
| Publication No. US20040175824A1
| Publication No. US20040175824A1
| APPLICANT: Sun, Lee-Hwei K
| APPLICANT: Sun, Lee-Hwei K
| APPLICANT: Sun, Cecily R
| TILLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
| TILLE OF INVENTION: activities
| FILLE REFERENCE: 025UN2001-A
| FILLE REFERENCE: 025UN2001-A
| FILLE REFERENCE: 0204-01-21
| FILLE PRICATION NUMBER: US/10/761,593A
| CURRENT FILING DATE: 2004-01-21
| PRIOR FILING DATE: 2001-08-17
| NUMBER OF SEQ ID NOS: 28
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 18
| LENGTH: 436
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sun, Bill N
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biologi
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biologi
FILE REPERENCE: 028UN2001
CURRENT APPLICATION NUMBER: US/09/932,812
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: HUEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure OTHER INFORMATION: A)
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232 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 291
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99.1%; Pred. No. 2.4e-48;
ive 1; Mismatches 0;
                                                                                                                                                                                                                                        Sequence 18, Application US/09932812
Publication No. US20030082749A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.1
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                     APPLICANT: Sun, Lee-Hwei K
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                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local Similarity 99.1
Matches 108; Conservative
  OTHER INFORMATION:
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COTHER INFORMATION:
US-10-800-497-18
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APPLICANT: Sun, Bill
APPLICANT: Sun, Bill
APPLICANT: Sun, Cecily
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor
TITLE OF INVENTION: biological activities
FILE REFERENCE: 03SUN2001
CURRENT APPLICATION WIMBER: US/09/968,362
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: hG-CSF-L-vFc gamma2 with a 30-amino acid leader peptide (Figure US-09-968-362-18
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                                                                                       1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
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; Bublication No. US20040259209A1
; GRUERAL INFORMATION:
   APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Etimulaing factor with
; TITLE OF INVENTION: Etimulaing factor with
; TITLE OF INVENTION: increased biological activities
; TITLE OF INVENTION: 105/10/800,497
; TITLE OF INVENTION: 2004-03-15
; CURRENT APPLICATION NUMBER: US/10/800,497
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR APPLICATION NUMBER: US/09/968,362
; ROOFWARE: Patentin version 3.1
; TENCHARE: Patentin version 3.1
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99.5%; Score 577; DB 10; Length 448;
Best Local Similarity 99.1%; Pred. No. 2.5e-48;
Matches 108; Conservative 1; Mismatches 0; Indels (
    Length 436;
                                           0; Indels
  Score 577; DB 20;
Pred. No. 2.4e-48;
1; Mismatches 0;
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US-09-968-362-18
IS-09-968-162-18

Sequence 18, Application US/09968362

Publication No. US20030082679A1

GENERAL INFORMATION:
Query Match
Best Local Similarity 99.1%;
Matches 108; Conservative
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ORGANISM: Artificial Sequence
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APPLICANT: Sun, Bill
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: FC fusion proteins of human granulocyte colony-stimulaing factor TITLE OF INVENTION: Increased biological activities
FILE REFERENCE: 03SUN2001
CURRENT APPLICATION NUMBER: US/10/800,449
CURRENT FILING DATE: 2004-03-15
PRIOR APPLICATION NUMBER: US/09/968,362
PRIOR APPLICATION NUMBER: US/09/968,362
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 448
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APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVERTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-30.
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: PCT/GB2004/004254
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-10-17
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                                                                                                                                    Length 448;
hG-CSF-L-vFc gamma2 with a 30-amino acid
peptide (Figure
2A)
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                                                                                                                                 99.5%; Score 577; DB 16; 99.1%; Pred. No. 2.5e-48; iive 1; Mismatches 0;
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; Sequence 18, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
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Query Match
Best Local Similarity 98.29
Matches 107; Conservative
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Matches 107; Conservative
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US-10-196-394-74
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US-10-370-749-16
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    US-10-277-370-3
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; Publication No. US20020004587A1
; GENERAL INFORMATION:
    APPLICANT: Willer, Kathy L.
    APPLICANT: MILEY, Leonard G.
    TILLE OF INVENTION: MULTIVALENT ANTIBODIES AND USES THEREFOR FILE REPERENCE: P1780R1
; CURRENT APPLICATION NUMBER: US/09/813,341
; CURRENT FILING DATE: 2001-03-20
; FRIOR PEDLICATION NUMBER: US 60/195,819
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NOS: 11
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                                                                                                                                                                   98.6%; Score 572; DB 18;
98.2%; Pred. No. 1.6e-48;
iive 1; Mismatches 1;
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Pred. No. 3.4e-48;
1; Mismatches 1;
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US-10-277-370-3
i Sequence 3, Application US/10277370
i Publication No. US20030157108A1
i GENERAL INFORMATION:
i APPLICANT: Presta, Leonard G.
i TILLE OF INVENTION: Glycoprotein Compositions
i FILE REFERENCE: P1877R1
CURRENT APPLICATION NUMBER: US/10/277,370
CURRENT APPLICATION NUMBER: US 60/337,642
i PRIOR FILING DATE: 2001-10-25
i PRIOR FILING DATE: 2001-10-25
i PRIOR FILING DATE: 2001-10-25
i PRIOR FILING DATE: 2001-10-69
i NUMBER OF SEQ ID NOS: 9
i SEQ ID NO 3
i LENGTH: 217
i TYPE: RRT
i ORGANISM: homo sapiens
                 SOFTWARE: Patentin version 3.3
SEQ ID NO 2
LENGTH: 109
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98.2%;
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Best Local Similarity 98.2
Matches 107; Conservative
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ORGANISM: Homo sapiens
                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-10-959-318-2
NUMBER OF SEQ ID NOS:
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Best Local Similarity
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98.6%; Score 572; DB 14; Length 217; 98.2%; Pred. No. 3.4e-48; ive 1; Mismatches 1; Indels
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98.2%; Pred. No. 3.4e-48;
iive 1; Mismatches 1;
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pred. No. 3.4e-48;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mark S. Dennis
TITLE OF INVENTION: Compounds that Bind HER2
FILE REFERENCE: P113M.
CURRENT APPLICATION NUMBER: US/10/196,394
CURRENT FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: US/09/609,721
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 74
LENGTH: 217
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 16, Application US/10370749
Publication No US20040002587A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Allan, Barrett
ITTLE OF INVENTION: FC Region Variants
FILE REFERENCE: AME-07823
CURRENT APPLICATION NUMBER: US/10/370,749
CURRENT PILION DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/358,161
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.2
LENGTH: 217
                                                                                                                                                                                                                                                                                                                                                                    Sequence 74, Application US/10196394
Publication No. US20030171278A1
GENERAL INFORMATION:
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Best Local Similarity 98.2%;
Matches 107; Conservative
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ORGANISM: Homo sapiens
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62 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 110
61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                              Search completed: November 17, 2005, 07:37:35
Job time : 84.6164 secs
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                                                                                                                                                                                                                                                                                Sequence 5, Application US/10835642

| Sequence 5, Application US/10835642
| Publication No. US200401912441
| GENERAL INFORMATION:
| APPLICANT: Leonard Presta |
| TITLE OF INVENTION: Polypeptide Variants with Altered Effector Function |
| FILE REPRENCE: P1726R1 |
| CURRENT APPLICATION NUMBER: US/10/835,642 |
| CURRENT FILING DATE: 2004-04-30 |
| PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/483,588 |
| PRIOR FILING DATE: EARLIER FILING DATE: 2000-01-14 |
| PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-15 |
| NUMBER OF SEQ ID NOS: 11 |
| LENGTH: 217 |
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TILE OF INVENTION: Polypeptide Variants with Altered Effector Function
FILE REPERENCE: P1726H: US/10/757,863
CURRENT APPLICATION NUMBER: US/10/757,863
CURRENT FILING DATE: 2004-01-15
PRIOR APPLICATION NUMBER: US 60/483,588
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/116,023
PRIOR APPLICATION NUMBER: US 60/116,023
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 5
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98.6%; Score 572; DB 16; Length 217;
Best Local Similarity 98.2%; Pred. No. 3.4e-48;
Matches 107; Conservative 1; Mismatches 1; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: homo sapiens
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US-10-835-642-5
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US-10-835-642-5
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Compugen Ltd.
GenCore version (c) 1993 - 2005
           Copyright
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sw model protein - protein search, using δ

Run on:

November 17, 2005, 07:11:49 ; Search time 89.0913 Seconds (without alignments) 473.187 Million cell updates/sec

US-09-674-857-2 score: Title: Perfect (

1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKTK 109 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

1206590

length: 0 length: 110 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_16Dec04:* L: geneseqp1980s:* 2: geneseqp1990s:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query			SUMMARIES	
Score Match	Length	8	ΠD	Description
2 98.6	109	7	AAR41709	Aar41709 Undefined
		'n	AAY54997	
562 96.9		'n	AAY54996	Aay54996 Mutated C
		m	AAY54998	Aay54998 Mutated C
		~	AAR67438	Aar67438 OKT3 mono
		~	AAR41717	Aar41717 Undefined
523 90.2	109	7	ADD25659	Add25659 Binding d
		~	AAR27680	Aar27680 Human imm
		~	AAR41684	Aar41684 Undefined
		œ	ADH75385	Adh75385 Human IgG
522 90.0		œ	ADJ52132	Adj52132 CH1 delet
		7	AAY42626	Aay42626 Human IgG
		S	AAE28089	_
		œ	ADH75415	Adh75415 CH2 regio
517 89.1		œ	ADL90103	_
		œ	ADH75413	Adh75413 CH2 regio
		6	ADD25761	Add25761 Binding d
		~	AAR41713	•
		œ	ADJ52129	Adj52129 CH1 delet
		~	AAW71023	Aaw71023 Mus muscu
		-	AAP83207	Aap83207 Sequence
		œ	ADL15711	
321 55.3	99	7	AAR75349	Aar75349 C-gamma-1
		7	AAR75351	Aar75351 C-gamma-1
		œ	ADL15713	Adl15713 Human imm

Sequence Sequence Sequence Sequence Sequence Sequence Human IgG Variant I Nariant I Variant I Va	Pig IgG2a Camel IgG Variant I
Aap83205 Aap83204 Aap83202 Aap83202 Aap83203 Aap833315 Adr59133 Adr59134 Aar33316 Aar33316 Aar33316 Aar593316 Aar593316 Aar59141 Aar59140 Adr59141	Adr59145 Adr59148 Aar33318
AAP83205 AAP83201 AAP83201 AAP83202 AAP83202 AAR33315 ADR59138 ADR59143 ADR59143 ADR59143 ADR59143 ADR59143 ADR59143 ADR3316 AAR33316 AAR3316 AAR3316	ADR59145 ADR59148 AAR33318
4444448888888888888	8 8 7
55 50 50 50 50 50 50 50 50 50 50 50 50 5	46 46 110
44444444444444444444444444444444444444	34.0 33.0 .200
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	197 197 192.5
00000000000000000000000000000000000000	4 4 4 6 4 0

ALIGNMENTS

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Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaccutical; gamma-3; gamma-4; diagnostic; agent; tumour; AlDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                                             Undefined ORF2 encoded by plasmid pAH4625
AAR41709 standard; protein; 109 AA
                                    (revised)
(first entry)
                                   25-MAR-2003
20-OCT-1993
                  AAR41709;
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Synthetic.

WO9310819-A1.

10-JUN-1993

92WO-US010206. 24-NOV-1992;

26-NOV-1991;

(ALKE-) ALKERMES INC.

Friden PM;

WPI; 1993-196742/24. N-PSDB; AAQ43846.

Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders.

Disclosure; Fig 17J; 151pp; English.

The sequences given in AAR41707-09 are encoded by the expression vector pAH4625. This vector represents the cloning of the human gamma isotype, gamma-2, with the variable region of the murine monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CHL, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones were isolated.

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This sequence represents the mutated CH2 molecule G2deltaa, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant domain of a human immunoglobulin G [IGS) heavy chain. The binding molecule is used to bind a target molecule (especially FcgammaRIIb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-va-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; encondata alloimmune thrombocytopaenia; docodpastures disease; therapy; sickle cell anaemia; coronary artery occlusion.
128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent eneurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                       1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                         APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
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                                                                                                                                                                                                                                                                                                                                                                         Length 109;
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                                                                                                                                                                                          Score 572; DB 2;
Pred. No. 1.6e-50;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutated CH2 sequence G2deltaa.
                                                                                                                                                                                              98.6%;
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                                                                                                                                                                                                              Local Similarity
                                                                                                                                                        Sequence 109 AA;
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AAY54997
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causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding of a second binding molecule, e.g. an antibody, to the target molecule. The binding molecule is useful for the treatment of graft-vg-host disease, organ transplant rejection, bone-marrow transplant cautoimmune thrombocytopaenia and arthritis), alloimmunity (e.g. tarcingmunity (e.g. tarcingmune thrombocytopaenia and arthritis), alloimmunity (e.g. total/neonatal alloimmune thrombocytopaenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN chromstal alloimmune thrombocytopaenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN chromary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through RegammaR and desirable complement or trigger cytotoxic activities through RegammaR and desirable immunogenicity. Further, they still bind Protein A, which is consistent immunogenicity. Further, they still bind Protein A, which is consistent with being able to cross the human placenta through interaction with FCRn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-vs-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; autoimmune disease; asthma; allergy; autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopaenia; doodpastures disease; therapy; sickle cell anaemia; coronary artery occlusion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVAGPSVFLFPPKPFDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 REEQFINSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 98.6%; Score 572; DB 3; Best Local Similarity 99.1%; Pred. No. 1.6e-50; Matches 108; Conservative 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY54996 standard; protein; 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutated CH2 sequence Gldeltaab.
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                                                                                                                                                                                                                                                                                                                                                   neonatal Fc receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-039075/03.
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9958572-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
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                        This sequence represents the mutated CH2 molecule Gideltaab, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (CD) an effector domain that is homologous to all or part of a constant domain of a human immunoglobulin G (IgG) heavy chain. The binding molecule is used to bind a target molecule (especially FegammaRIIb causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule is useful for the transplant rejection, autoimmune thrombocytopaenia and arthritis, autoimmune harmolytic anaemia, catoimmune thrombocytopaenia and arthritis), alloimmunity (e.g. vaculitis, autoimmunity (e.g. catoing and arthritis), alloimmunity (e.g. corplement or trigger cytotoxic activities through Fegamma and allergy), corporary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through Fegamma and corporation acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent immunogenically and are therefore likely to have reduced immunogenically alloids, and are therefore likely to have reduced immunogenically alloids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Binding molecule, CH2 sequence, complement dependent lysis, FogammaRIID; cell-mediated destruction, human; immunoglobulin G; IgG heavy chain; B cell activation, mast cell degranulation; phagocytosis, vasculitis; Crohn's disease; graft-va-host disease; organ transplant rejection, alloimenument edisorder; autoimmune haseolytic anaema; inflammatory disease; autoimmune thrombocytopaenia; arthritis; erythroblastosis foctalis; neonatal alloimmune thrombocytopaenia; decodpastures disease; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPVAGPSVFLFPPKDKDTLMISRTFEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.9%; Score 562; DB 3; Length 109; 95.4%; Pred. No. 1.7e-49; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sickle cell anaemia; coronary artery occlusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY54998 standard; protein; 110 AA
Claim 12; Fig 17; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutated CH2 sequence Gldeltaac.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (neonatal Fc receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY54998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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This sequence represents the mutated CH2 molecule Gldeltaac, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without tringering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (CD) an effector domain that is homologous to all or part of a constant combined in the comprises: (b) an effector domain that is homologous to all or part of a constant combined in the comprises of B cell activation, mast cell degranulation or phagocytosis). The binding molecule of second binding molecule, e.g. an antibody, to the target complexity of a second binding molecule, e.g. an antibody, to the target complexity of a second binding molecule, e.g. an antibody to the target complexity of a second binding molecule, a such meaning to the target of graft-vs. The binding molecule is useful for the treatment of graft-vs. The binding molecule is useful for the treatment of graft-vs. The control molecule and arthritis, alloimmunity (e.g. autoimmune thrombocytopaenia and arthritis), alloimmunity (e.g. autoimmune thrombocytopaenia and arthritis), alloimmunity (e.g. chronic or acute inflammatory diseases (e.g. Crohn's HDN corronary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FogammaR and desirable thouse main amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Portein A, which is consistent immunogenicity. Further, they still bind Portein A, which is consistent with being able to cross the human placenta through interaction with FCRn contracts.
                                                                                                                                                                                                Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVAGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monoclonal antibody; antibody engineering; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 PREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.2%; Score 540.5; DB 3; Length 110; 93.6%; Pred. No. 2.7e-47; ive 4; Mismatches 2; Indels 1;
(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                               Williamson LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR67438 standard; protein; 109 AA.
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                                                                                                                                                                                                                                                                                                                                  Claim 12; Fig 17; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.2%;
Best Local Similarity 93.6%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (neonatal Fc receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                           Clark MR,
                                                                                                                                 WPI; 2000-039075/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             humanized antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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08-JUL-1995
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                                                                                                                                                                                                                                                                properties.
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The sequences given in AAR41715-18 are encoded by the expression vector pAH4808. This vector represents the cloning of the human gamma isotype, gamma 4, with the variable region of the murine monoclonal antibody camma isotype, campoint the the variable region of the murine monoclonal antibody in which the eavy chain (VH) is derived from a murine source and the sequences encoding CHI, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AQ43845), was transfected into SD2/0 cells and clones were isolated. Is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding domain; immunoglobulin; fusion protein; cytostatic; antiatrbritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; Immunoglobulin heavy chain; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent coll-mediated cytotoxicity; ADCC; complement fixation; antigon; exercinoma; sarcoma; rheumatoid archritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDFEVQENWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Binding domain-immunoglobulin fusion protein-associated protein #107.
                                                                           diagnosis and treatment of cancer, AIDS and neurological disorders.
                                                   Antibody conjugates specific for transferrin receptor - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.4%; Score 536; DB 2; Length 110; 94.3%; Pred. No. 7.7e-47; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 OFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 GFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                         Disclosure; Fig 19J; 151pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD25659 standard; protein; 109
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
       N-PSDB; AAQ43848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 110 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                      The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) has potent T-cell activating and immunosuppressive activity, and is used to treat transplant patients to prevent rejection. The antibody can be engineered to contain a human Fc region. By transferring the binding specificity into a human framework, the immunogenicity is reduced without affecting the immunosuppressive activity. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AlbS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                                                                                                                                                                                                                                                     New humanised OKT3 antibody with mutated Fc receptor binding region - useful as immunosuppressant to reduce transplant rejection, lacks the T-cell activating side effects of wild type antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 OFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 536; DB 2;
Pred. No. 7.6e-47;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Undefined ORF2 encoded by plasmid pAH4808,
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 82-87; 135pp; English.
                                                                                                                                              Jolliffe L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR41717 standard; protein; 110 AA
  94WO-US006198
                                                 93US-00070116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.4%;
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 94.3
Matches 100; Conservative
                                                                                                                                              Bluestone JA, Zivin RA,
                                                                                               (ARCH-) ARCH DEV CORP
                                                                                                                                                                                               WPI; 1995-022721/03.
                                                                                                                                                                                                                         P-PSDB; AAQ75356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 109 AA;
01-JUN-1994;
                                                 01-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUN-1993
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Query Match

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Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

(GENE-) GENECRAFT INC.

(ALKE-) ALKERMES INC

26-NOV-1991;

Synthetic

AAR41717;

RESULT

WPI; 1993-196742/24.

Friden PM;

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Gaps

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63 64

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In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17. The inventor's propose eliminating these allotypes by amino acid changes to agree with the sequences of IgG2, IgG3 and IgG4. None of the allotype sites (1, 2 and 17) are located within the CH2 domain. New "isoallotypes" should be suitable for therapeutic use in all patients. See AAR27678-R27681. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised antibodies having modified allotypic determinant - useful for matching allotypes in therapy with decreased likelihood of causing undesirable immune responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light; chain; variable; constant; region; anti-human; transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE
                                             Isoallotype; IgG1 Glm(1,2,17); anti-allotype response; humanised Ab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.2%; Score 523; DB 2;
90.6%; Pred. No. 1.6e-45;
tive 6; Mismatches 4;
Human immunoglobulin IgG1 CH2 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR41684 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Undefined ORF2 encoded by pAH4602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4c; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92WO-US010206.
                                                                                                                                                                                                                                           92WO-GB000445.
                                                                                                                                                                                                                                                                                        91GB-00005245.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                        (LYNX-) LYNXVALE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-349162/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 110 AA;
                                                                                                                                                                                                                                                                                        12-MAR-1991;
                                                                                                Homo sapiens
                                                                                                                                           WO9216562-A1
                                                                                                                                                                                                                                           12-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9310819-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
20-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR41684;
                                                                                                                                                                                                                                                                                                                                                                                        Clark MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                           The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide, an immunoglobulin heavy chain Comperising a binding region polypeptide, an immunoglobulin heavy chain CCC immunoglobulin heavy chain CH2 constant region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide comprises, where the mutated human IgG1 immunoglobulin hinge region polypeptide companies, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains of contains 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains to polypeptide contains of a least one of the mutated human IgG1 immunoglobulin hinge region polypeptide contains of cysteine residues. The binding domain immunoglobulin hinge region polypeptide contains of cysteine residues. The binding domain immunoglobulin hinge region polypeptide contains or cysteine residues. The binding domain immunoglobulin hinge region polypeptide contains or cysteine residues. The binding domain immunoglobulin hinge region polypeptide contains or cysteine residues. The binding domain immunoglobulin hinge region polypeptide contains or construct. Compisated the polymclectide (operably linked to a pronocent construct compisate the polymclectide opymerising the binding domain-immunoglobulin fusion protein, a recombinant expression construct. Producing the binding domain-immunoglobulin fusion protein or polymclectide and a carrier, and treating a subject having or suspected of having a mailgannt condition or a B-cell disorder, e.g. malanoma, carrier, and rearting a mailgannt condition or a B-cell disorder, e.g. malanoma, carrier, and carrier, and restring sequence of the seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
                                          New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.2%; Score 523; DB 7; Length 109; 90.6%; Pred. No. 1.6e-45; ive 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                           Disclosure; SEQ ID NO 220; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR27680 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
WPI; 2003-801317/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 109 AA;
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10-MAR-1993
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RESULT 8
AAR27680
ID AAR2
XX
AC AAR2
XX
DT 25-M
XX
XX

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63 64

Gaps

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Length 110; 4; Indels

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The invention relates to a new composition comprises a variant of a parent polypeptide having at least a portion of a FC region. The variant mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells more effectively than the parent polypeptide and comprises at least one amino acid medification at position 280 in the Ex region. The composition is useful in treating diseases e.g., autoimmune diseases. The present sequence represents the amino acid sequence of a human immunoglobulin G, IgG, CH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CH1 deleted mimetibody; osteopathic; cardiovascular-Gen; dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytocataic; antiinflammatory; neuroleptic; ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; nose disorder; oral disorder; dermatological disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; endocrine disorder; hepatic disorder; obstetric disorder; haematologic disorder; mumunological disorder; allergic disorder; infectious disorder; musculoskeletal disorder; oncological disorder; neurological disorder; neurological disorder; popthalmologic disorder; pediatric disorder; pediatric disorder; pediatric disorder; pediatric disorder; popthalmologic disorder; pediatric disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE
                                                                                                                                  New composition comprising a variant of a parent polypeptide having least a portion of a Fe region, useful in treating e.g., autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CH1 deleted mimetibody-related CH2 peptide SeqID1124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 523; DB 8;
Pred. No. 1.6e-45;
6; Mismatches 4
                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 23; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ52132 standard; protein; 102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           renal disorder; pulmonary disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 90.2%;
1 Similarity 90.6%;
96; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2003; 2003WO-US020495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                Watkins JD, Allan B;
                                                                                  WPI; 2004-070755/07.
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Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 110 AA;
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                                                                                                                                                                                        diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAR41682-85 are encoded by the expression vector, pAH4602. This vector contains open reading frames encoding the heavy chain variable region (WH) of the antibody 128.1, an ampicialin resistance gene and a histidine (histidinol) selection marker.

Transcription of the VH gene is from the VH promoter of the murine 27.44 gene. The vector also includes a heavy chain immunoglobulin enhancer and the human gammal constant region (CH). The VH region of 128.1 was colieved by polymerase chain reaction and cloned into plasmid pAH4274.

This was achieved by digesting the plasmid and the product with EcoRV and Nhel. The VH gene was inserted in-frame with the human gammal CH region CH at the 3' end of the VH-J region by means of a Nhel site. 128.1 is an ceptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuro-pharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent charkingons and Alzheimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                             Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC; autoimmune disease; human; IgG; immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.2%; Score 523; DB 2; Length 110; 90.6%; Pred. No. 1.6e-45; ive 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                          Disclosure, Fig 11K; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH75385 standard; protein; 110 AA.
     91US-00800458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2003; 2003US-00370749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human IgG1 CH2 region.
                                                  (ALKE-) ALKERMES INC
                                                                                                                                                        WPI; 1993-196742/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                             N-PSDB; AAQ43844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS2004002587-A1
26-NOV-1991;
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                                                                                                     Friden PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH75385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches

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28-JUN-2002; 2002US-0392431P. 19-SEP-2002; 2002US-0412144P.

20-FEB-2002; 2002US-0358161P

(WATK/) WATKINS J D. (ALLA/) ALLAN B.

(CENZ) CENTOCOR INC

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Gaps

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4; Indels

Length 110;

64

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AAE28089;
                                                                                                                                                                                                                                                                                                                           diseases
                  Jardieu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                  which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen, gastrointestinal-Gen, grantolitory, endocrine-Gen, gastrointestinal-Gen, grantolitory, endocrine-Gen, gastrointestinal-Gen, grantolitory, endocrine-Gen, grantolitory memoralists, memoratory in enroleptic, ophthalmological, mephrotropic or respiratory-Gen activity acting as a tumour necrosis factor (TNF)-modulator or cytokine-agonist. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the CH1 deleted mimetibody, such as a bone or joint, cardiovascular, dental or oral, dermatological, ear, nose or throat, candorine, metabolic, gastrointestinal, gynaecological, hepatic, obstetric, haematologic, immunological, allergic, infectious, musculoskeletal, oncological, neurological, nutritional, ophthalmologic, pediatric, psychiatric, renal or pulmonary disorders. The present cequence is that of a CH2 peptide which may be used during the creation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                           This invention relates to CH1 deleted mimetibodies (and the DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS
                                                                                    diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic and nutritional disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin B; IgE; antagonist; FcepsilonRI receptor; human; bds;
receptor-binding; binding determinant sequence; anti-IgE antibody;
allergic disease.
                                                                       nucleic acid, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
 Scallon BJ, Nesspor TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 522; DB 8; Length 102;
Pred. No. 1.9e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                       deleted mimetibody polypeptide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                              Claim 7; SEQ ID NO 1124; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human IgG1 Fcgammal-Fcgamma2 residues
 Ghrayeb J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY42626 standard; protein; 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-00178583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 96.1
nes 98; Conservative
 Knight DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                           WPI; 2004-082872/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 102 AA;
Heavner GA, Kutoloski KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68
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                                                                       CHI
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Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia; vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial; immunosuppressive; lymphoid malignancy; respiratory syncytial virus; anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides immunoglobulin E (IgE) antagonists comprising one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified immunoglobulins useful in the treatment of autoimmune diseases,
                                                                                        Immunoglobulin E variants as peptide antagonists useful for raising and screening anti-immunoglobulin E (IgE) antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment of allergic
                                                                                                                                                                                                                                                                         or more of the FoepsilonRI receptor-binding determinant sites of buman 1gE. The antagonists include 1gE variants comprising an immunoglobulin template and binding determinant sequences (bds) CDD6a, BFbds and the sequence shown in AAY42581. The CDbds (CD loop binding determinant sequences) are selected from the sequences shown in AAY42567-Y42577 and the BFbds (BF loop binding determinant sequence) are selected from sequences shown in AAY4258-Y42580. The variants are useful in raising and screening anti-1gE antibodies, in the isolation and purification of PcepsilonRI receptor and in the treatment and prophylaxis of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.0%; Score 522; DB 2; Length 105; 92.3%; Pred. No. 1.9e-45; ive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 NSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE28089 standard; protein; 109 AA
                                                                                                                                                                                                           Claim 7; Col 63-64; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-2000; 2000US-0254884P.
09-MAY-2001; 2001US-0289760P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-2001; 2001WO-US048432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 92.3%;
Matches 96; Conservative
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Presta LG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MEDI-) MEDIMMUNE INC
                                              WPI; 1999-579941/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dall'acqua W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-DEC-2002
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Indels

Length 110;

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The present invention relates to a method for generating an immune response to an antigen in a patient. The method comprises administering to the patient an immunoglobulin (ig) or its portion where the Ig has at least one peptide epitope of the antigen attached to the Ig or its portion and administering the immunoglobulin or its portion in conjunction with a RNA segment. A recombinant human Ig molecule capable of binding to an FC gamma receptor (FogammaR) of an antigen presenting cell (APC) was used to illustrate the invention. The recombinant human Ig molecule comprises a CH3 region (ADL90102), a CH2 region (ADL90103), a hinge region (ADL90104) and a flanking peptide (ADL90105).
                                                                                                                                                                                           S LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTSPREE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VAGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generating an immune response to an antigen, useful for generating desired T cell responses comprises administering an immunoglobulin one peptide epitope of the antigen attached to the immunoglobulin.
                                                                                                                                                                                                                                                                           64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immune response; immunoglobulin; Ig; CH2 region; human.
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Pred. No. 6.7e-45;
                                                                Score 518; DB 8; Le
Pred. No. 5.3e-45;
                                                                                                                        6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                ADL90103 standard; protein; 110
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89.6%;
                                                                                  89.3%;
ilarity 89.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-295415/27.
                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ASTR-) ASTRAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                           Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004027049-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                        95;
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    variant
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Matches
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                                                                                            The invention relates to a modified immunoglobulin (IgG1) which comprises in IgG constant domain having at least one amino acid modification. The immunoglobulins are used in the treatment or prevention of a disease or disorder by passive immunotherapy for vaccinating a subject and for in vivo diagnosis of a subject. The disease and disorders include a gamma globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versushost, lymphoid malignancies and passive immunotherapies and also for the treatment of various systemic infections. The present sequence is human immunoglobulin GI (IgG1) Fc region second constant (CH2) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a new composition comprises a variant of a parent polypeptide having at least a portion of a Fc region. The variant mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells more effectively than the parent polypeptide and comprises at least one amino acid modification at position 280 in the Fc region. The composition is useful in treating diseases e.g., autoimmune diseases. The present sequence represents a CH2 region
                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
comprises at least one amino acid modification relative to a wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VAGPSVFLFPPKPKDTLMISRIPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                     Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                              3, Indels
                                                                                                                                                                                                                                                                                                                                                     Score 518; DB 5;
Pred. No. 5.2e-45;
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                                                          Disclosure; Page 138; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH75415 standard; protein; 110 AA
                   immunoglobulin constant domain
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l Similarity 91.3%;
95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watkins JD, Allan B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WATK/) WATKINS J D.
(ALLA/) ALLAN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-070755/07.
                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                              Sequence 109 AA;
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RESULT 14

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Gaps

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Indels

Length 110;

diseases

63 64

having

Thu Nov 17 11:27:16 2005

ò g Search completed: November 17, 2005, 07:47:00 Job time : 90.0913 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
               Copyright
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- protein search, using sw model OM protein November 17, 2005, 07:37:49; Search time 16.4247 Seconds (without alignments) 638.529 Million cell updates/sec Run on:

US-09-674-857-2 580 Title: Perfect score:

1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKTK 109 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

44790 Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 110

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Iq qamma-2b chain	IgE_chain C3 regio	chain C3	psilon c	Ig kappa chain Cr	appa c	ambda	Ig lambda chain C	Ig lambda-5 chain	Ig lambda-1 chain	Ig lambda chain C	Ig lambda-2 chain	Ig lambda-5 chain	. Ig light chain C r	Ig lambda chain C	Ig kappa-1 chain C	Ig kappa chain C r	Ig kappa-B4 chain	Ig lambda chain C	Ig lambda chain C	Ig lambda chain C	Ig lambda chain C	Ig lambda chain -	Ig kappa chain C r	Ig lambda-1 chain	Ig kappa chain C r	Ig kappa-2 chain C	Ig kappa-B4 chain	lambda-chain C-reg
ID	A30503	168726	168730	843147	КЗНО	S26653	B30554	B26167	B26434	LIMS	L2HU	S22760	800259	B34509	S26654	F53275	A37927	K4RB	H32529	L1PG	I50740	L7RB	IS0741	KSRBV	A27390	K1MS	K4RBBS	G20907	146731
DB	0	~	7	7	-	~	~	~	~	-	-	~	~	~	7	Ŋ	7	-	7	-	~	-	~	-	7	Н	7	~	7
* Query Match Length	88	107	107	110	106	66	105	103	105	105	105	106	106	102	86	104	66	103	105	105				104	105	106	106	106	102
& Query Match	47.8	25.2	25.2	23.4	23.3	22.6	22.5	22.1	21.5	0	0	20.8	20.6	•	19.7	19.4	19.1	18.9	18.4	18.0	17.8	17.7	17.6	17.2	17.2	17.2	16.6	16.6	16.1
Score	277	146	146	136	135	131	130.5	128	124.5	120.5	120.5	120.5	119.5	118	114.5	112.5	111	109.5	106.5	104.5	103	102.5	102	100	100	100	96	96	93.5
Regult No.	1	7	3	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

168726

Tige chain C3 region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

C;Accession: 168726

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C;Accession:

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-107 <RES>
A;Cross-references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM>

A; Accession: 168726

Ig kappa chain C r Ig kappa-B9 chain Ig lambda-2 chain Ig kappa-B5 chain Ig light chain C r Ig kappa chain C r Ig lambda-3 chain Ig lambda-2 chain Ig lambda-2 chain Ig lambda-2 chain Ig lambda-2 chain Ig lambda-2 chain Ig lambda-2 chain Ig lambda-2 chain Ig lambda-2 chain Ig lambda-2 chain	gamma-3 ch
KIRTB K9RB K9RB K5RB K1RTA L3MS S22762 D34509 PL0186 PL0186 PL0186 S2652 PL0186	A24629
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v.v.v.u.o.g.g.4.u.v.v.v.u.n	90
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ALIGNMENTS

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Ig gamma-2b chain C region (ES.7A12) - mouse (fragment)
C,Species: Mus musculus (house mouse)
C,Date: 31-Mar-1989 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 SRIPEVICVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDW
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-70/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                  A,Accession: A30503
A,Molecule type: mRNA
A,Residues: 1-88 cdll.>
A,Cross-references: GB:M21925
A,Experimental source: myeloma cell line MPC11
A,Note: the authors translated the codon GAG for residue 41 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Indels
                                                                C,Accession: A30503
R,Gllmore, G.L.; Bard, J.A.; Birshtein, B.K.
J. Immunol. 141, 1754-1761, 1988
A;Title: DNA rearrangements affecting both variable and A;Reference number: A30503; MUID:88315788; PMID:2842402
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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A; Molecule type: protein A; Residues: 1-106 <GOT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgE chain C3 region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: 168730
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid A;Reference number: 154443; MUID:88152907; PMID:3346043
A;Accession: 168730
A;Status: preliminary; translated from GB/EMBL/DDBJ
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S43147

G19 upsilon chain - duck (fragment)

C;Species: Anas platyrhynchos (domestic duck)

C;Species: Anas platyrhynchos (domestic duck)

C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000

C;Accession: S43147

R;Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.

Submitted to the EMBL Data Library, March 1994

A;Description: Evidence from duck immunoglobulin genes that IgY is the common ancestor

A;Reference number: S43145
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                                                                                                                                                                          6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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    Length 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A,Residues: 1-107 <RES>
A,Cross-references: GB-M22933; NID:g194464; PIDN:AAA37915.1; PII
C,Superfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 < MAG5
A;Cross-references: EMBL:X78355; NID:g468612; PID:g468613
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                         48; Indels
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    ; DB 2;
1.1e-07;
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25.2%; Score 146; DB 33.0%; Pred. No. 1.1e-ive 19; Mismatches
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Query Match
Best Local Similarity 33.09
Matches 34; Conservative
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Matches 37; Conserv
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Best Local Similarity
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ig kappa chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: 31-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004 C;Accession: B90562; A31651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02 R;Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M. Biochemistry 9, 3155-3161, 1970 A;Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequenc A;Contents: myeloma protein Eu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Cross-references: UNITROT: P01834
A/Cross-references: UNITROT: P01834
A/Cross-references: UNITROT: P01834
A/Cross-references: UNITROT: P01834
A/Sociali, W.B.s.; Edelman, G.M.
Biochemistry 9, 3188-1196, 1970
A/Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid A/Edference number: A90565; MUID: 170640327; PMID: 4923144
A/Contents: annotation; Eu. Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z.: Physiol. Chem. 353, 189-208, 1972
A/Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Subg A/Reference number: A91651; MUID: 22188439; PMID: 5027703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A91651
A;Nolcoule type: protein
A;Residues: 1-106 <SUT>
R;Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
Cell 22, 197-207, 1980
A;Tille: Cloned human and mouse kappa immunoglobulin constant and J region genes conserve A;Fille: Cloned human and mouse Pappa immunoglobulin constant and J region genes conserve A;Reference number: A90806; MUID:81042304; PMID:6775818
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A;Residues: 1-56,'Q',58-106 <HI2>
R;Titani, K.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 244, 3550-3560, 1969
A;Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete E: A;Reference number: A)2047; MUID:69234734; PMID:4893682
A;Contents: Bence Jones protein Ag
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A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Rossidues: 1-106 cHIE>
A,Cross-references: GB:J00241; NID:g33140; PIDN:CAA23823.1; PID:g1335148
A,Note: the sequence was determined from the germline gene
A,Note: the sequence was determined from the germline gene
R;Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, In Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74, A;Reference number: A94417
A;Contents: Bence Jones protein Roy
A;Accession: A94417
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: Latt, A,A6-56, Q',58-82, L',84-106 cHIL>
A;Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu
R;Hilschmann, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
A;Title: Die volstaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).
A;Reference number: A91639; MUID:68242259; PMID:5586923
A;Contents: Bence Jones protein Cum
A;Accession: A91639
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A; Residues: 1-13,'N',15-106 <TIT>
R; Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.
Science 169, 56-59, 1970
A; Title: Macroglobulin structure: variable sequence of light and heavy chains.
A; Reference number: A94242; MUID:70201507; PMID:5447531
A; Contents: Waldenstrom's macroglobulin Ou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 1-13,'N',15-106 <KOH>
R;Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
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C;Accession: B26434
R;Sakaguchi, N.; Melchers, F.
Rskaguchi, N.; Melchers, F.
Asture 324, 579-582, 1986
A;Title: Lambda-5, a new light-chain-related locus selectively expressed in pre-B lympho A;Reference number: A26434; MUID:87065143; PMID:3024017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPRE 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PKSAPSVTLFPPSKEE--LDTNKATVVCLISD--FYPGSVNVVWKADGSIINQNVKTTQA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: B26167 E.; Lentner, F.; Tel-Or, S.; Burstein, Y.; Schechter, I. EMBO J. 6, 97-102, 1987 Ariticle: Analyses of chicken immunoglobulin light chain cDNA clones indicate A;Reference number: A26167; MUID:87218480; PMID:3107981
         C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 21-May-1988 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 22.1%; Score 128; DB 2; Length 103; Best Local Similarity 29.0%; Pred. No. 7e-06; Matches 31; Conservative 26; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;COSB-references: UNIPROT:P20763; GB:M33049
A;Note: 90-Asp was found in one cDNA clone
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heteroteramer; immunoglobulin
F;21-87/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                            compared with conceptual translation
                                                                                                                                                                                                                                                                                                                       A;Residues: 1-105 <POL>
(Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;20-88/Domain: immunoglobulin homology <IMM>
                                                                                                                         J. Immunol. 142, 708-711, 1989
A;Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A;Reference number: A30554; MUID:89093962; PMID:2492052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 22.5%; Score 130.5; I
1 Similarity 29.6%; Pred. No. 4e-06
32; Conservative 23; Mismatches
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Ig lambda-5 chain C region - mouse
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A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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A;Residues: 1-105 <SAK>
                                                                           C; Accession: B30554
R; Foley, R.C.; Beh,
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S26633
Ig kappa chain C region - chimpanzee (fragment)
C;8pecies: Pan troglodytes (chimpanzee)
C;8pecies: Pan troglodytes (chimpanzee)
C;Becies: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C;Accession: 826653
R;Bhrish, P.H; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A;Title: Potennial of primate monoclonal antibodies to substitute for human antibodies:
A;Reference number: 826652; MUID:91355693; PMID:2129418
A;Recensialtion not shown
A;Molecule type: mRNA
A;Residues: 1-99 < ERNA
A;Residues: 1-99 < ERNA
A;Cross-references: EMBL:X65287
C;Superfanily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Map position: 2p12-2p12

C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-88/Domain: immunoglobulin homology <IMM>
F;26-86/Disulfide bonds: #status experimental
F;106/Disulfide bonds: interchain (to heavy chain) #status experimental
Am. J. Hum. Genet. 48, 613-620, 1991
A,Title: Km typing with PCR: application to population screening.
A,Reference number: A37927; MUD:91150772; PMID:1900145
A,Accession: B37927; MUD:91150772; PMID:1900145
A,Accession: B37927; MUD:91150772; PMID:1900145
A,Accession: B37927
A,Accession: B37927
A,Accession: B37927
A,Molecule type: DNA
A,Molecule type: DNA
A,Accession to compared with conceptual translation
A,Residues: 8-10c - KUR
A,Note: allocype Inv(3)
B,Steiner, V.; Chang, J.Y.
B,Steiner, V.; Chang, J.Y.
A,Title: Chemical modification of the carboxyl groups of protein substrates enhances the A,Reference number: S02572; MUD:88005152; PMID:3115831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAAPSVFIFP--PSDEQLKSGTASVVCLINNFYPREAKVQ--WKVDNALQSGNSQESVTE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VAGPSVFLFFPFKPTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGV--EVHNAKTKPR 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: GDB:IGKC
A,Cross-references: GDB:120088; OMIM:147200
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Ig lambda chain C region - sheep (fragment)
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Best Local Similarity 31.1:
Matches 33; Conservative
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Matches 33; Conserv
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a few germl

us-09-674-857-2.LL.rpr

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Cispecies: Homo sapiens (man)
Cibate: 31-Jan-1981 #sequence revision 31-Jan-1981 #text change 09-Jul-2004
Cibate: 31-Jan-1981 #sequence revision 31-Jan-1981 #text change 09-Jul-2004
Ciracces 32057; A90243; A91970; A91650; A90375; B90381; A93268; A02125
Rittani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 245, 2171-2176, 1970
A;Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete A;Reference number: A20267; MulD: 70166723; PMID: 4909564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A92057
A;Anclecule type: protein
A;Residues: 1-105 < TIT>
A;Residues: 1-105 < TIT>
A;Cross-references: UNIPROT: P01842
B;A;Cross-references: UNIPROT: J 1842
B;Cross-references: UNIPROT: J 1863
B;Cross-references: UNIPROT: J 1863
B;Cross-reference unaber: A90243; MUID: 69088380; PMID: 4883841
A;Contents: Bence Jones protein X; disulfide bonds
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A;Contents: Bence-Jones protein Nig-64
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A/Molecule type: protein
A/Residues: 1-105 CxAM>
A/Residues: 1-105 CxAM>
A/Residues: 1-105 CxAM>
A/Residues: 1-105 CxAM>
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A;Residues: 1-44,'G',46-105 <PON>
A;Note: this sequence has the Kern+ marker, 45-Gly (instead of Ser)
B;Chen, B.L.; Poljak, R.J.
Biochemistry 13, 1295-1302, 1974
A;Title: Amino acid sequence of the (lambda) light chain of a human myeloma immunoglobulin
A;Reference number: A90375; MUID:74109553; PMID:4814727
A;Contents: myeloma protein Newm; partial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: A90375
A,Molecule type: protein
A,Residues: 1-81, Kr, 83-105 < CHE>
A,Residues: 1-81, Kr, 83-105 < CHE>
A,Residues: 1-81, Kr, 83-105 < CHE>
A,Residues: 1-81, Kr, 83-105 < CHE>
A,Note: this chain has the Oz+ marker, 82-Lys (instead of Arg)
R,Poljak, R. J.; Amzel, L. Mr, Avey, H.P.; Chen, B.L.; Phizackerley, R.P.; Saul, F.
B,Fotc. Natl. Acad. Sci. U.S.A. 71, 3440-3444, 1974
A,Title: The three-dimensional structure of the Fab' fragment of a human myeloma immunogl
A,Reference number: A93788; MUID:75046825; PMID:4215080
A,Contents: annotation; Newm; X-ray crystallography, 2.0 angstroms
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A;Residues: 1-4, 'N', 6,'T', 8-44,'G',46-55,'K',57-105 <FET>
A;Note: this sequence has the Kern+ marker, 45-Gly, and the Mcg+ marker, 5-Asn, 7-Thr, ar
R;Edmundson, A.B.; Ely, K.R.; Abola, E.E.; Schiffer, M.; Panagiotopoulos, N.
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A;Residues: 1-105 <MIL>
R;Kametani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
J. Biochem. 93, 421-429, 1983
                                                                       2 PKSSPSVTLFPPSSEEL----ETNKATLVCTITDFYPGVVTVDMKVDGTFVTGMETTOP 57
     61
     PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEV-HNAKTKPR
                                                                                                                                                                                                                                                                                             SB SKQSNNKYMASSYLTLTARAWERHSSYSCQVTHEG--HTVEKSLSR 101
                                                                                                                                                                                                                                 62 EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISK 107
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A;Title: Primary structure of the Mcg lambda chain.
A;Reference number: A90381; MUID:75013804; PMID:4415202
A;Contents: Bence Jones protein Mcg; partial sequence
A;Accession: B90381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lambda chain C regions - human
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 31-Mar-1981 Hasquence revision.
C;Accession: A93922; A93221; A92126
C;Accession: A93922; A93221; A92126
E;Selsing, E.; Miller, J.; Wilson, R.; Storb, U.
Proc. Natl. Acad. Sci. U.S.A. 79, 4681-4685, 1982
A;Title: Evolution of mouse immunoglobulin lambda genes.
A;Reference number: A93922; MUDD:83014953; PMID:6812053
A;Molecule type: DNA
A;Residues: 1-105 < SEL>
A;Cross-references: UNIPROT:PO1843; GB.J00587; NID:g197754; PIDN:AABS9672.1; PID:g197761
A;Residues: 1-105 < SEL>
A;Cross-reference number: A93251; MUD:81148806; PMID:6259534
A;Accession: A93251
A;Accession: A93251
A;Accession: A93251
A;Accession G lambda genes in the MOPC-315 plasmacytoma.
A;Reference number: A93251; MUD:81148806; PMID:6259534
A;Accession: A93251
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A;Accession G lambda genes in the mopc-315 plasmacytoma.
A;Accession: A93251
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A; Residues: 1-105 < B02>
A; Residues: 1-105 < B02>
A; Residues: 1-105 < B02>
A; Mopella, E.
R; Appella, E.
R; Appella, E.
A; Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
A; Reference number: A93775; MUID: 71107854; PMID: 527667
A; A; Contents: myeloma protein MOPC 104E
A; Accession: A93775
A; Molecule type: protein
A; Residues: 1-18, TE', 21-55, E', 57-74,76-80, SH', 83-85,'S', 86-95,'Q', 97-105 < APP>
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into lates and a subunits associate into lates and a subunits associate into lates and a subunits associate into lates and a subunits associate into lates and a subunits associate into lates and a subunity immunoglobulin C region; immunoglobulin homology
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A;Title: Somatic variants of murine immunoglobulin lambda light chains.
A;Reference number: A93282; MUID:82220143; PMID:6283385
A;Contents: S43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKSDPLVTLFLPSLKN-LQPTR-PQLVCLVSE--FYPGTLVVDWKVDGVPVTGGVETTQP 57
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                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                               A,Note: the authors translated the codon TAC for residue 84 as C,Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKQTNNKYMVSSYLTLISDQMMPHSRYSCRVTHEG--NTVEKSVS 100
                                                                                                                                                                                                                                                                           Query Match 21.5%; Score 124.5; DB 2; Length 1 Best Local Similarity 31.4%; Pred. No. 1.6e-05; Matches 33; Conservative 25; Mismatches 40; Indels
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20; Mismatches 48; Indels
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A;Cross-references: GB:M30387
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Mus genus:

gene in the

7:

Length 106; Indels .

DB 2;

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C;Accession: S26654
R;Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A;Title: Potential of primate monoclonal antibodies to substitute for human antibodies: A;Reference number: S26652; MUID:91355693; PMID:2129418
A;Accession: S26654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEV-HNAKTKPR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 PKSDPLVTLFLPSLKNL----QANKVTLVCLVSEFYPGTLVVDWKVDGVPVTQGVETTQP 58
                                   Ig lambda-5 chain C region - western wild mouse C;Species: Mus spretus (western wild mouse) C;Species: Mus spretus (western wild mouse) C;Date: 31-Dec-1988 #sequence_revision 07-Sep-1990 #text_change 21-Jan-2000 C;Accession: S0029 C;Accession: Accession: Kindt, T.J. Cazenave, P.A.; Kindt, T.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig light chain C region 3 - sandbar shark (fragment)
C;Species: Carcharhinus plumbeus (sandbar shark)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 17-Nov-2000
C;Accession: B34509
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C.Species: Pan troglodytes (chimpanzee)
C.Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
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Proc. Natl. Acad. Sci. U.S.A. 86, 9961-9965, 1989
A;Title: Evolution of immunoglobulin light chains: cDNA clones specifying
A;Reference number: A34509; MUID:90099382; PMID:2513577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-102 <SCH>
A;Residues: 1-102 <SCH>
A;Cross-references: GB:M29044; NID:g212941; PIDN:AAA49153.1; PID:g212942
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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                                                                                                                                                                                                        EMBO J. 7, 117-122, 1988

Afitie: Conservation of the immunoglobulin C-lambda-5 gene in the Afitie: Conservation of the immunoglobulin C-lambda-5 gene in the Afities of Conservation of the immunoglobulin translation
Affactus inct compared with conceptual translation
Affactus inct compared with conceptual translation
Affactus inct compared with conceptual translation
Affactus incompared with conceptual translation
Affactus incompared with conceptual translation
Affactus in immunoglobulin C region; immunoglobulin homology
C; Keywords: hererotetramer; immunoglobulin
F; 21-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTIS 106
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20.6%; Score 119.5; DB 2
Best Local Similarity 29.5%; Pred. No. 5.2e-05;
Matches 31; Conservative 23; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNTFSVSSYLTLSASDWNSHELYSCLVKHEAL 101
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          S00259
Ig lambda-5 chain C
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Best Local S
Matches 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Gene: GDB:IGLC2; IGLC
A; Cross-references: GDB:12691; OMIM:147220
A; Cross-references: GDB:12691; OMIM:147220
A; Cross-references: GDB:122691; OMIM:147220
A; Cross-references: GDB:122411.2-22411.2
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Superfamily: immunoglobulin homology < IMM>
F; 20-88/Domain: immunoglobulin homology < IMM>
F; 21-86/Disulfide bonds: #status experimental
F; 104/Disulfide bonds: interchain (to heavy chain) #status experimental
Biochemistry 14, 3953-3961, 1975

A;Title: Rotational allomerism and divergent evolution of domains in immunoglobulin ligh A;Title: Rotational allomerism and divergent evolution of domains in immunoglobulin ligh A;Reference number: A0391

A;Contents: annotation; Mcg; X-ray crystallography, 2.3 angstroms

R;Hieter, P.A.; Hollis, G.F.; Korsmeyer, S.J.; Waldmann, T.A.; Leder, P. Nature 294, 536-540, 1981

A;Title: Clustered arrangement of immunoglobulin lambda constant region genes in man. A;Reference number: A93268; MUD:82080680; PMID:6273747

A;Accession: A93268

A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:CAA41312.1; PID:g51764
                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-105 <HIE>
A;Cross-references: GB:J00253; NID:g186118; PIDN:AAA59107.1; PID:g186127
A;Note: six tandem lambda-type genes were identified and the three most 5' were sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
S22760
[12] lambda-2 chain C region - mouse (fragment)
C; Species: Wus musculus (house mouse)
C; Species: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C; Accession: S2276
R; Weiss, S.; Wu, G.E.
EMBO J. 6, 927-932, 1987
A; Title: Somatic point mutations in unrearranged immunoglobulin gene segments encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ce (lambda-3)
C;Comment: The sequence shown is the Kern-/Oz-/Mcg- chain found in proteins Sh, X,
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEV-HNAKTKPR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKSSPSVTLFPPSSEL----ETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEG--STVEKTVAPTE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-106 <WEID
A;Cross-references: UNIPROT:09D8W4; EMBL:XS8411; NID:g51763; PII
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: hetercetramer; immunoglobulin
F;21-89/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.8%; Pred. No. 4.1e-05; ive 25; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.8%; Score 120.5;
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A;Status: translation not shown
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Matches 30; Conservative
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sandbar shark

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Gaps

97

RESULT 13

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3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVH-NAKTKPR 61
                                                                                                                                                                                                                                                                  2 PKAAPSVTLFPPSSEE--LQANKATLVCLISD--FYPGAVTVAWKADSSPVRAGVETTTP 57
                                                                                                                                                                                                         7; Gaps
                                                                                                                                                              Query Match 19.7%; Score 114.5; DB 2; Length 98; Best Local Similarity 29.1%; Pred. No. 0.00015; Matches 30; Conservative 21; Mismatches 45; Indels
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-98 <EHR>
A;Cross-references: EMBL:X65286
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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Search completed: November 17, 2005, 07:55:07 Job time: 16.4247 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: November 17, 2005, 07:13:34 ; Search time 77.1461 Seconds

(without alignments)

723.518 Million cell updates/sec

Title: US-09-674-857-2
Perfect score: 580
Sequence: 1 APPVAGPSVFLFPPKPXDTL......CKVSNKGLPSSIEKTISKTK 109

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5 Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 301588

Minimum DB seq length: 0 Maximum DB seq length: 110 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P01834 homo sapien	P20763 gallus gall		<u>-</u>	homo	_	P20764 mus musculu	P01840 oryctolagus			P03984 oryctolagus	P20766 rattus norv	P01837 mus musculu	P01839 oryctolagus		P01838 oryctolagus		P01841 oryctolagus	ratt	anm	mue	_		Q6ezi5 bacillus an	P79659 oncorhynchu	P79660 oncorhynchu	Q31248 peromyscus	Q30837 ovis aries		_	Q61bv9 mus musculu
SUMMAKIES	. QI	KAC HUMAN	LAC_CHICK	QatGus	LAC1 MOUSE	LAC HUMAN	LACS MUSSP	LAC5 MOUSE	KAC4_RABIT	LAC PIG	LAC_RABIT	KAC6 RABIT	LAC1_RAT	KAC MOUSE	KACB RABIT	KACB RAT	KAC9_RABIT	LAC2 RAT	KAC5 RABIT	KACA_RAT	LAC3_MOUSE	LAC2 MOUSE	099JC1	Q8KYI0	Q6EZI5	P79659	P79660	Q31248	Q30837	SNSP HUMAN	Q8FBY4	Обгвия
	DB	្ន	٦	~	٦	-	П	٦	٦	Н	ч	Н	Н	Н	-	Н	н	Н	Н	н	Н	Н	~	0	7	7	7	7	7	Н	7	7
	Query Match Length	106	103	106	105	105	105	105	103	105	105	104	104	106	106	106	104	104	103	106	104	104	105	107	107	74	74	91	104	79	73	93
de	Query Match	23.3	22.1	21.3	20.8	20.8	20.6	19.9	18.9	18.0	17.7	17.2		17.2	16.6	15.9	15.5	15.5	15.2			13.6	13.6	11.6	11.6	11.3	11.3	10.9	10.8	10.7	10.5	10.5
	Score	135	128	123.5	120.5	120.5	119.5	115.5	109.5	104.5	102.5	100	100	100	96	92	90	90	88	87	86	79	79	67	67	65.5	65.5	63	62.5	62	61	61
	Result No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

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P79661 Q6LBW2	Q8HB97 Q768W8	041412 Q9JKP1	Q7XZF9	Q649X2	031261	P79652 P79657	019471	019472
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74 93	102	92	86	100	106	4 4	93	93
10.4	10.3	10.3	10.2	10.2	10.2	101	10.1	10.1
60.5	59.5	59 59 59	0.0	50	5 20	 	58.5	58.5
33	334	36 37	38	4.0	41	4 4 2 4	44	45

ALIGNMENTS

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                                                                                             MEDLINE=69234734; PubMed=4893682;
Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. 3. The
complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3560(1969).
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515; Olsen R.E., Sletten K., Westermark P.; Sletten K., Westermark P.; Sterended analysis of Al-amyloid protein from abdominal wall subcutaneous fat biopsy: kappa IV immunoglobulin light chain."; Biochem. Biophys. Res. Commun. 245:713-716(1998).

-I- MISCELLANBOUS: The EU sequence has the INV (3) allotypic marker, Ala-45 and Val-83. The ROY sequence has the INV (1,2) allotypic marker, Ala-45 and Leu-83.

-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
  "The complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00047, 1g; 1. _-
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
3D-8tructure; Direct protein sequencing; Immunoglobulin C region;
                                                                                                                                                                                                                 SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
MEDLINE=70201507; PubMed=5447531;
Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interchain (with a heavy chain).
V -> L (in INV(1,2) marker).
FTIG=VAR 003897.
D -> N (in Ref. 7 and 8).
E -> Q (in Ref. 5 and 6).
                                      Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig-like.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-33; 38-41 AND 62-80.
                                                                             SEQUENCE (BENCE-JONES PROTEIN AG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB; 1D5B; X-ray; A/L=1-103.
PDB; 1D5I; X-ray; L=1-103.
PDB; 1D6V; X-ray; L=1-103.
PDB; 1HEZ; X-ray; L=1-106.
PDB; 1HZ; X-ray; L=1-106.
PDB; 117Z; X-ray; A/C=1-106.
PDB; 1MM; X-ray; L=1-105.
Genew; HGNC:5716; IGKC.
HINVDB; HIX0021121; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J00241; AAA58989.1; -.
                                                                                                                                                                                                                                                                                                                   Science 169:56-59(1970).
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86
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106
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                                                                                                                                                                                                                                                                                                                              4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGV--EVHNAKTKPR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=87218480; PubMed=3107981;
Parvari R., Ziv E., Lentner F., Tel-Or S., Burstein Y., Schechter I.;
"Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germline V lambda genes and allotypes of the C lambda locus.";
EMBO J. 6:97-102(1987).
-:- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
15 lambda chain.
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                          Gaps
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SWART; SW00407; iGc]; 1.
PROSITE; PS0835; IG_LIKE; 1.
PROSITE; PS00299; IG MHC; 1.
Immunoglobulin C region; Immunoglobulin domain; Polymorphism.
                                                                                                                                                                                                                                                 23.3%; Score 135; DB 1; Length 106; 31.1%; Pred. No. 9.5e-06; ive 26; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     62 EEQPNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISK 107
                                                                                                                                                                                                                                                                                                                                                                                                                             Interchain (with heavy chain).
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1, 11609 MW; 51984DIFDD372CE8 CRC64;
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77BF341B511B91B2 CRC64;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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Best Local Similarity 31.1%;
Matches 33; Conservative
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103 AA;
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LAC_CHICK
ID__LAC_CHICK
AC__P20763;
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                                                                                                                                                                          3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPRE
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                                                                                     Gaps
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hyporhetical protein DKFp667J0810 (Fragment).
Name=DKFp667J0810;
Hyporhetical protein DKFp667J0810 (Fragment).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[11]
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                             63 EQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                           Length 103;
                                                                               44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bair A., Lauber J., Mewes H.W., Weil B., Amid C., Osange Han M., Wiemann S.,
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AL713(SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AL713(SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMSPP, P01842; 1LIL.
InterPro: IPR00310110; Ig-like.
InterPro: IPR003597; Ig_cl.
InterPro: IPR003597; Ig_cl.
Effam; PF07654; Cl.set; I.
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                     22.1%; Score 128; DB 1; 29.0%; Pred. No. 4.6e-05; iive 26; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Ig lambda-1 chain C region.
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PROSITE; PS00290; IG MHC; UNKNOWN_1.
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The German cDNA Consortium;
                                                                               31; Conservative
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                  Query Match
Best Local Similarity
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AC PO1843;
DT 21-JUL-1986
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DT 21-JUL-1986
DT 21-JUL-1986
DC 21-JUL-1986
DC Mus musculus
CC Mammalia; EU
CX NCBI_TAXID=1
RN [1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apprair acid sequences of two mouse immunoglobulin lambda chains.";
Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
-!- MISCELLANEOUS: The MOPC 315 cell line produces 2 light chains, 1
normal lambda-2 chain and 1 abnormal lambda-1 chain that is
missing a large part of the V region. The C region sequence (shown
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EMBL; J00587; AAB59672.1; -..
EMBL; J00587; AAB59672.1; -..
EMBL; J00587; AAB59672.1; -..
EDB; L1MS; A=1-105.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
Pfam; PF0047; ig; Ig-MHC.
PROSITE; PS00290; IG_MHC; 1..
PROSITE; PS00290; IG_MHC; 1..
DROSITE; PS00290; IG_MHC; 1..
IMMUNOGlobulin domain.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                              "Somatic variants of murine immunoglobulin lambda light chains.";
                                                                                                                                                               MEDIJUE-81148806; PubMed=6259534;
Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
Gefter M.L., Baltimore D.;
"Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
                                                                                                                                                                                                                                                                                                                                         MEDLINE-82220143; PubMed-6283385;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
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Q -> E (in Ref. 4).
Missing (in Ref. 4).
HS -> SH (in Ref. 4).
S -> SS (in Ref. 4).
E -> Q (in Ref. 4).
SEQUENCE FROM N.A.
MEDLINE=33014953; PubMed=6812053;
Selsing E., Miller J., Wilson R., Storb U.;
"Evolution of mouse immunoglobulin lambda genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685 (1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE (MYELOMA PROTEIN MOPC 104E). MEDLINE=71107854; PubMed=5276767;
                                                                                                                                                SEQUENCE FROM N.A. (MOPC 315)
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (S43).
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"Structural rule of antibodies. Primary structure of a monoclonal
immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
protein Kern). V. The complete amino acid sequence and its genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-69088380; PubMed-4883841;
Milstein C., Clegg J.B., Jarvis J.M.;
"Immunoglobulin lambda-chains. The complete amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Comparative studies on the structure of the light chains of human immunoglobulins. IV. Assignment of a subsubgroup."; J. Biochem. 93:421-429(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Titani K., Wikler M., Shinoda T., Putnam F.W.;
"The amino acid sequence of a lambda type Bence-Jones protein.
complete amino acid sequence and the location of the disulfide
                                                                                                                                                                                               20.8%; Score 120.5; DB 1; Length 105; 29.2%; Pred. No. 0.00027;
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Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                         62 EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISK 107
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MEDLINE=74109253; Pubmed=4814727;
Chen B.L., Poljak R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE (BENCE-JONES PROTEIN NIG-64).
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MEDLINE=71150336; PubMed=5549568;
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Biochem. J. 110:631-652(1968),
                                                                                                                                                                                                                                                          Conservative
  Homo sapiens (Human)
64
75
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105 AA;
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-!- MISCELLANBOUS: The sequence shown is the Kern-/Oz-/Mcg- chain found in proteins 8H, X, and NIG-64. The Kern protein has the reart marker, the NEWM protein has the Oz+ marker, the Mcg protein has the Kern+ marker, and the Mcg+ marker.

-!- MISCELLANBOUS: Six tandem lambda-type genes were identified and the 3 most 5' were sequenced. These correspond to the Mcg sequence (lambda-1), the Kern-/Oz- sequence (lambda-2) and the Kern-/Oz+ sequence (lambda-3).

-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Edmundson A.B., Ely K.R., Abola B.E., Schiffer M., Panagiotopoulos N.;
"Rotational allomerism and divergent evolution of domains in
immunoglobulin light chains.";
Biochemistry 14:3953-3961(1975).
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Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
"Clustered arrangement of immunoglobulin lambda constant region genes
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MEDLINE=90133913; PubMed=2515285;
Bly K.R., Herron J.N., Harker M., Edmundson A.B.;
"Three-dimensional structure of a light chain dimer crystallized in water. Conformational flexibility of a molecule in two crystal forms.";
acid sequence of the (lambda) light chain of a human myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=75046825; PubMed=4215080;
Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
Saul F.,
                                                                                                                                                SEQUENCE (DOT).
MEDLINE=95255298, PubMed=7737190;
Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri "Characterization of the two unique human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The three-dimensional structure of the fab' fragment of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=75013804; PubMed=4415202;
Fett J.W., Deutsch H.F.;
Pett Jarinary structure of the Mcg lambda chain.";
Biochemistry 13:4102-4114(1974).
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X51754; CAB38569.1; ALT_INIT.
X51755; CAA36049.1;
                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 228:886-893(1995)
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                                 immunoglobulin (IgG New).";
Biochemistry 13:1295-1302(1974)
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PDB; 1LIL; X-ray; A/B=1-105.
PDB; 2MCG; X-ray; -.
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X51755; CAA36049.1;
X51755; CAA36051.1;
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Nature 345.579-582(1986).
-! - TISSUB SPECIFICITY: Selectively expressed in pre-B lymphocytes.
-! - SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=87065143; PubMed=3024017;
Sakaguchi N., Melchers F.;
"Lambda 5, a new light-chain-related locus selectively expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 Interchain (with heavy chain) 11674 MW; AAB417DF68471A17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKQTNNKYMVSSYLTLISDQMMPHSRYSCRVTHEG--NTVEKSVS 100
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                                 -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1. 5. 5MART; SM0047; ig; 1. 5. 5MART; SM00407; IGc1; 1. PROSITE; PS0035; IG LiKE; 1. PROSITE; PS00290; IG MHC; 1. Immunoglobulin C region; Immunoglobulin domain. NON TER 1 IG 100 Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.6%; Score 119.5; DB 1
29.5%; Pred. No. 0.00033;
iive 23; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-5D-1UL-2004 (Rel. 44, Last annotation update)
IG lambda-5 chain C region.
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HSSP; P01843; 1JNH.
                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                  EMBL; M35582; AAA39152.1; -.
HSSP; P01843; 1JNH.
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            7:117-122(1988)
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104 1
105 AA;
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ses 31; Conserv
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P20764;
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Mami F., Cazenave P.A., Kindt T.J.;
"Conservation of the immunoglobulin C lambda 5 gene in the Mus gene.";
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01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g lambda-5 chain C region.
Mus spretus (Western wild mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musine, Musine.
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                                                                                                                                       GO: GO: 0003823; F: antigen binding; NAS.
GO: GO: 0006955; P: immune response; NAS.
InterPro: IPR007100; Ig-like.
InterPro: IPR0071006; Ig-MHC.
Pfam: PF00047; ig; 1.
PROSTIE; PS50835; IG-LIKE; 1.
PROSTIE; PS00290; IG-MHC; 1.
3D-structure; Bence-Jones protein; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interchain (with heavy chain).
A - N (in MCG+ marker).
FTIG=VAR_003898.
S - T (in MCG+ marker).
/FTIG=VAR_003899.
S - S (in Kern+ marker).
/FTIG=VAR_003900.
T - K (in MCG+ marker).
T - K (in MCG+ marker).
FTIG=VAR_003901.
R - K (in CZ+ marker).
/FTIG=VAR_003902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:5855; ICLCI.
Genew; HGNC:5856; IGLC2.
Genew; HGNC:5857; ICLC3.
H-InvDB; HIX0016285; -.
MIM; 147220; -.
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Best Local Similarity
Matches 30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                 3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEV-HNAKTKPR 61
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"Primary structure of the L chain from a rabbit homogeneous antibody to streptococcal carbohydrate. II. Sequence determination of peptides from tryptic and peptic digests.";
J. Biol. Chem. 250.3289-3296(1975).
-I- MISCELLANBOOUS: This chain was obtained from antibody to the specific carbohydrate of group C Streptococci and was isolated from the serum of a single rabbit.
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MEDLINE=83300036; PubMed=6412231;
Emorine L., Dreher K.L., Kindt T.J., Max E.E.;
"Rabbit immunoglobulin kappa genes: structure of a germline b4 allotype J-C locus and evidence for several b4-related sequences in the rabbit genome.";
Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
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MEDLINE-82060334; PubMed-6795636;
Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
"Nucleotide sequence of constant and 3' untranslated regions of a kappe immunoglobulin light chain mRNA of a homozygous b4 rabbit.";
Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-1986 (Rel. 44, Last annotation update)
19 kappa-b4 chain C region.
10 kappa-b4 chain C region.
Oryccolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                        19.9%; Score 115.5; DB 1; Length 105; 30.5%; Pred. No. 0.00084; tive 25; Mismatches 41; Indels 7
                                                                                                                                                                                                                                          104 Interchain (with heavy chain).
11678 MW; 1F210915904A86A5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                           SMART; SM00407; IGC1; 1-PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG MHC; FALSE NEC.
Immunoglobulin C region; Immunoglobulin domain.
NON TER A
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                  InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig_MHC.
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hes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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86
104
MGD; MGI:96529; Igl-5.
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104
105 AA;
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DISULFID
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                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PVA-PTVLIFPPAADQ--VATGTVTIVCV---ANKYFPDVTVTWEVDGTTQTTGIENSKT
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"Amino acid sequence of normal (microheterogeneous) porcine
immunoglobulin lambda chains.";
Blochemistry 16:3765-3772(1977).
-!- MISCELLANEOUS: This chain was obtained from a mixture of normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 103;
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                                                                                                                                                                                                                                                                                                                            Interchain (with a heavy chain)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 P--QNSADCTYNLSSTLTLTSTQYNSHKEYTCKVT-QGTTSVVQ 96
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                   5 95 1g-like.
26 85 103 Interchain (with a heavy c
103 103 Interchain (with a heavy c
58 58 N -> D (in Ref. 3).
103 AA; 11043 MW; SPCSACCBB60E68DB CRC64;
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                         PERM: PO0047; ig; 1.
PROSITE: PS50835; IG_LIKE; 1.
PROSITE: PS00290; IG_MHC; FALSE NEG.
Direct protein sequencing; Immunoglobulin C region;
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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HSSP; P01842; 2MCG.
InterPro; IPR001310; Ig-like.
InterPro; IPR0013597; Ig c1.
InterPro; IPR003506; Ig_MHC.
Pfam; PF00047; Ig; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                HSSP; P01837; 1KCV.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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27.5%;
EMBL; X00231; CAA25051.1; -. PIR; A93971; K4RB.
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105 AA;
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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104
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                                                                 2 PKAAPIVNLFPPSSBEL----GINKAILVCLISDFYPGAVIVTWKAGTIVTQGVETIKP 57
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                                       3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNA--KTKP
  Gaps
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID=9986;
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23-OCT-1986 (Rel. 02, Last sequence update)
25-DAN-2005 (Rel. 46, Last annotation update)
1g kappa chain b5 variant C region.
Oryccolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  imminoglobulin lambda-chains.";
Biochem. J. 197:177-183(1981).
-!- MISCELLANEOUS: This lambda chain expresses the c7 allotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=82091105, PubMed=6797414;
Garcia I., Jaton J.-C.;
"The primary structure of the constant region of Basilea-rabbit
9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                          61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                  -SKOSNNKYAASSYLALSASDWKSSSGFTCQVTHEG--TIVEKTVTPSE 103
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11484 MW; B427513272E8663D CRC64;
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49; Indels
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HSSP; P01842; LTRB.
HSSP; P01842; LAQK.
HSSP; P01842; LAQK.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_MC.
InterPro; IPR003597; Ig_Li.
InterPro; IPR003597; Ig_MHC.
SWART; SW0407; Ig_I.
PROSITE; PS00290; IG_MHC; PALSE_NEG.
Direct protein sequencing; Immunoglobulin C region;
Immunoglobulin domain.
NON_TER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specificity.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
01-FBB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 lambda chain C region.
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.7%; Score 102.5; DB 25.7%; Pred. No. 0.017;
                                                                                                                                                                                                                                                                       105 AA
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21; Mismatches
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30; Conservative
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105 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Emorine L., Sogn J.A., Trinh D., Kindt T.J., Max E.E.;
"A genomic gene encoding the b5 rabbit immunoglobulin kappa constant region: implications for latent allotype phenomenon.",
proc. Natl. Acad. Sci. U.S.A. 81:1789-1793 (1984).

-!- MISCELLANBOUS: The cDNA from which this sequence was derived contains a terminator codon within the V-region coding region. The origin of this codon and of the differences between this and other sequenced b5 C regions are unclear. The cDNA clone was made using mRNA from trypanosome-infected b5-homozygous rabbits.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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SEQUENCE FROM N.A. (CLONE PKB5-F2).
MEDLINE=84041515; PubMed=6314281;
Bernstein K.E., Skurla R.M. Jr., Mage R.G.;
Bernstein K.E., Skurla R.M. ijn in thains of b4 and b5 allotypes
differ more in their constant regions than in their 3' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interchain (with a heavy chain)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 EQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSS0835; IG LIKE; 1.
PROSITE; PS00290; IG WHC; FALSE NEG.
Immunoglobulin C region; Immunoglobulin domain.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.2%; Score 100; DB 1
25.7%; Pred. No. 0.03;
tive 25; Mismatches
                                                                                                                                                                           regions.";
Nucleic Acids Res. 11:7205-7214(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig-like.
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EMBL; K01363; AAA31355.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02124; KSRBV.
HSSP, P01837; 25C8.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 11.
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 PVAGPSVFLFPPKPKDTLMISRTPEVT--CVVVDVSHEDPEVQ-FNWYVDGVEVHNAKTK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                       MEDLINE-87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2; Steen M.L., Hellman L., Pettersson U.; "The immunoglobulin lambda locus in rat consists of two C lambda genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE (MOPC 21).
MEDLINE=73053310; PubMed=4638343;
Sasti J., Milstein C.;
"The complete amino acid sequence of a mouse kappa light chain.";
Biochem. J. 128:427-444(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFIDE BONDS (MOPC 21).
MEDLINE=73008889; PubMed=5073237;
Svasti J., Milstein C.;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 TQPFKQNNKYMATSYLLLTAKAWETHSNYSCQVTHE--ENTVEKSLSRAE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 104;
                                                                                                                                                                                                                                                                                                                                                                                     Interchain (with heavy chain)
                                                                                                                                                                                                                                                                                                                                                                                                                     17.2%; Score 100; DB 1; Length 10
26.4%; Pred. No. 0.03;
tive 23; Mismatches 46; Indels
                                                                                          and a single V lambda gene.";
Gene 55:75-84(1987).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                104 AA; 11565 MW; CBF71811F4BC878A CRC64;
                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_MHC.
Pfam: PF00047; ig_l.
SMART; SM00407; ig_l.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin C region; Immunoglobulin domain.
NON_TER
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21-JUL-1986 (Rel. 01, Last sequence update)
22-CCT-2004 (Rel. 45, Last annotation update)
1g kappa chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 AA
                                                                                                                                                                                                                                                                                                                                                            Ig-like.
                                                                                                                                                                                                                                  EMBL; M22520; AAA41419.1; ALT_INIT.
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                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             HSSP; P01843; 1JNH
                        VCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-81191915; PubMed-6262318; Max B.E., Maizel J.Y. Jr., Ledder P.; Max B.E., Maizel J.Y. Ur., Ledder P.; Mithe nucleotide sequence of a 5.5-kilobase DNA segment containing the mouse kappa immunoglobulin J and C region genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-81199949; PubMed=6785724;
Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;
"DNA sequence of the constant gene region of the mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88329081; PubMed=3118116; de Waele P., Fiers W.; de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.; "Expression in non-lymphoid cells of mouse recombinant immunoglobulin
                                                                                                                                                                                                                                                                                                            MEDLINE=82059477; PubMed=6170937; Hamlyn P.H., Gait M.J., Milstein C.; "Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxymuclectide method of RNA sequencing."; Nucleic Acids Res. 9:4485-4494(1981).
SEQUENCE FROM N.A., AND REVISIONS TO 53-59.

MEDLINE-19084137; PubMed=103625; DOI=10.1016/0092-8674(78)90290-8; Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.; "Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the dideoxynucleotide method of RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00407; ĪGcl; 1.
PROSITE; PSE0828; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
3D-structure; Direct protein sequencing; Immunoglobulin C region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              directed against the tumour marker human placental alkaline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eur. J. Biochem. 176:287-295(1988).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kappa chain.";
Nucleic Acids Res. 9:971-981(1981)
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PDB; IKCR; X-ray; L=1-106.
PDB; IKCV; X-ray; L=1-106.
PDB; ICCV; X-ray; L=1-106.
PDB; ICCV; X-ray; A=1-106.
PDB; IORQ; X-ray; A=1-106.
PDB; IORQ; X-ray; A=1-106.
PDB; DSG; X-ray; L=1-103.
MGD; MGI:96495; IgCC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00047; ig; I.
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1FSK; X-ray; B/E=1-106
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L=1-106.
                                                                                                                                                                                 sequencing.";
Cell 15:1067-1075(1978)
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DISULFID
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                                                                                                                                                                                                          5 AGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNA--KTKPRE 62
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is lambda. The kappa chain shown is a minor component. All other rabbit B allotypes have Cys-64.
                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Heidmann O., Rougeon F.; "Multiplicity of constant kappa light chain genes in the rabbit genome: a byb4 homosygous rabbit contains a kappa-bas gene."; EMBO J. 2:437-441(1983).
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9
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                                                                                                                                                                       17.2%; Score 100; DB 1; Length 106; 24.3%; Pred. No. 0.03; ive 25; Mismatches 50; Indels
                                                                                                                                                       11778 MW; 4B51FF5EF49BAEB5 CRC64;
                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
18 Kappa-b4 chain C region.
                                                                                                                                                                                                                                                                                                          106 AA
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; V01241; CAA24558.1; -.
EMBL; V00885; -; NOT_ANNOTATED_CDS.
PIR; A02121; K4RBBS.
HSSP; P01837; 25C8.
                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR007110; Ig-like.
InterPro, IPR003006; Ig_MHC.
                                                                                                                                                                    Query Match
Best Local Similarity 24.3'
                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                               103
106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Basilea;
PubMed=11894960;
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                        RABIT
                                                                                                                                                       SEQUENCE
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P01839;
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                                                                                                                                                                                                                                                                                                                                                             3 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVE----VHNAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interchain (with a heavy chain).
D - N (in Ref. 2).
N - K (in Ref. 2).
Missing (in Ref. 2).
E -> Q (in Ref. 2).
E -> Q (in Ref. 2).
V -> W (in Ref. 2).
S -> N (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 KPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POSPE--DNIYSLSSTLSLTSAQYNSHSVYTCEVV-QGSASPIVQSFNR 103
                                                                                                                                                       27 87
106 106 Interchain (with a heavy chain).
106 AA; 11279 MW; AF9B928DDA853849 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The primary structure of a rat kappa Bence Jones protein: phylogenetic relationships of V- and C-region genes."; J. Immunol. 115:59-62(1975).
-! SIMILARITY: Contains 1 immunoglobulin-like domain. PIR; A93901; KIRTB.
INSP: POR 198037, 10R8.
InterPro; IPR00310; Ig-like.
InterPro; IPR003597; Ig_c1.
                                                                                                                                                                                                                                                          Length 106;
                                                                                                                                                                                                                                                          Query Match 16.6%; Score 96; DB 1; Length 106
Best Local Similarity 28.4%; Pred. No. 0.076;
Matches 31; Conservative 22; Mismatches 44; Indels
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SMART; SM0047; ig; 1.
SMART; SM00407; IGG1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
Direct protein sequencing; Immunoglobulin C region;
NON TER.
Pfam; PF00047; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; FALSE NEG.
Immunoglobulin C region; Immunoglobulin domain.
DOWĀIN 6 99 Iq-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Kappa chain C region, B allele.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 AA.
                                                                                                                                     Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig-like
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MEDLINE-75212238; PubMed=807630;
Starace V., Querinjean P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Louvain;
MEDLINE=82082587; PubMed=6273908;
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87
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6; Gaps
                                                                                                      Query Match
15.9%; Score 92; DB 1; Length 106;
Best Local Similarity 22.4%; Pred. No. 0.19;
Matches 24; Conservative 28; Mismatches 49; Indels
SQ SEQUENCE 106 AA; 11601 MW; 4CFA7CA820D1CA36 CRC64;
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Search completed: November 17, 2005, 07:52:16 Job time: 78.1461 secs

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Sequence 30, Application US/0844644

Patent No. 6015555

GENERAL INFORMATION:

APPLICANT: Friden, Phillip M.

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER LEADABLE FORM:
MEDIUM TYPE: Riopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/44,644
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/44,646
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1999
ATPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1999
ATPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1999
ATPLICATION NUMBER: US 07/404,089
FILING DATE: UFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK86
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 109 amino acids
amino acid
                        TYPE: amino acid
TOPOLOGY: linear
USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                             1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKTK 109
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1: /cgn2 6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2 6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2 6/ptodata/1/laa/5A_COMB.pep:*
4: /cgn2 6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2 6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/1/laa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-444-644-30

US-08-23-246A-30

US-08-57-050-4

US-08-444-644-44

US-08-432-246A-44

US-08-232-246A-21

US-08-232-246A-31

US-08-222-101-10

US-08-862-101-10

US-08-422-091-10

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US-09-490-153-166
US-09-490-324-166
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                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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580
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Match Length
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107
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Maximum DB seq length: 110
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No.
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ALK88-15AAAZ

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Sequence 40, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 13, Appli
Sequence 7, Appli
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Sequence 6, Appli
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                 S-08-761-277A-49
S-08-444-644-26
S-08-232-246A-26
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US-08-422-091-8
US-08-422-092-8
US-08-422-093-8
US-08-422-093-8
US-08-422-112-8
US-09-301-593-20
US-09-313-942-13
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US-08-378-939-42
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US-08-436-463-8
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COUNTRY:
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US-08-557-050-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30, Application US/08232246A
Patent No. 6329508
GENERAL INFORMATION:
GENERAL INFORMATION:
FITTLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
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                                                                                                                                                     Length 109;
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                                                                                                                                                                                                                     1; Indels
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CARDUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: El PR PC COMPAIDE.
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,65077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTONNEY/AGENT INFORMATION:
NAMR: MARNEY: US-DATA:
AARDANEY/AGENT INFORMATION:
NAMR: WARNEY: US-DATA:
NAMME: WARNEY: US-DATA:
NAMME: WARNEY: US-DATA:
NAMME: WARNEY: US-DATA:
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NAMME: WARNEY: US-DATA:
NAME:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                              98.6%; Score 572; DB 3; 98.2%; Pred. No. 1.7e-59;
                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REPERENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMUNICATION INFORMATION:
TELEPAX: (617) 861-6240
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 109 amino acids
amino acid
GY: linear
                                                                                                                                          Query Match
Best Local Similarity 98.2
Matches 107; Conservative
       protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein FRAGMENT TYPE: internal
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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-444-644-30
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1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60

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                                                                                                                                                                                                                                                                     Sequence 1. Application US/08070116A

Patent No. 5885573

GENERAL INFORMATION:

APPLICANT: 21vin, Robert A.

APPLICANT: Joulife, Linda K.

APPLICANT: Bluestone, Jeffrey A.

TITLE OF INVENTION: Methods and Materials For Modulation

TITLE OF INVENTION: Of the Immuno-suppressive Activity and

TITLE OF INVENTION: Toxicity of Monoclonal Antibodies

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSER: AARNOId, White & Durkee

STREET: P.O. Box 4433

CITY: Houston
                                                                                                                           61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                       61 REEQFINSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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Patent No. 6491916
EDBERAL INFORMATION:
APPLICANT: Bluestone, Jeffrey A.
APPLICANT: Zivin, Robert A.
APPLICANT: Jobliffe, Linda K.
APPLICANT: MODULATION OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 92.4%; Score 536; DB 2; Length 109; Best Local Similarity 94.3%; Pred. No. 2.8e-55; Matches 100; Conservative 3; Mismatches 3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/07,116A
PILING DATE: 01-JUN-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION UNDHER: ARCD:082
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (512) 418-3000
TELEFRAX: (512) 444-7577
INFORMATION E CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States of America
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Техав
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77210
                                                                                                                                                                                                                                                               US-08-070-116A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-070-116A-4
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4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phillip M.
TRANSFERIN RECEPTOR SPECIFIC
TRANSFORY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.4%; Score 536; DB 3; Length 110; 94.3%; Pred. No. 2.8e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-232-246A-44

Sequence 44, Application US/08232246A

Sequence 44, Application US/08232246A

Patter No. 632950B

GENERAL INFORMATION:

TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC

TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTHODY-NEUROPHARMACEUTICAL OR DIAN

TITLE OF INVENTION: ANTHODY-NEUROPHARMACEUTICAL OR DIAN

TITLE OF INVENTION: ANTHODY-SEPONDENCES 46

CORRESPONDENCE ADDRESS:

ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Lexington

CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 04-MAY-1994
CLASSIFICATION: 530
                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                            FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION 1424
PRIOR APPLICATION 100 DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR DATE: 07-SEP-1990
PRIOR DATE: 07-SEP-1990
PRIOR DATE: 07-SEP-1990
PRILING DATE: 07-SEP-1990
ATTORNEY/AGENT INFORMATION:
                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
          OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 110 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 94.3
Matches 100, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-444-644-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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     THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL ANTIBODIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 44, Application US/08444644

Patent NO. 6015555
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCES A6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 2.8e-55;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-LUSS/MS-LUOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,050
FILING DATE: Concurrently Herewith
CLASSITCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06198
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/070,116
FILING DATE: 01-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAMME: Wilson, Mark B.
REGISTRATION NUMBER: ARCD:208
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 414-7577
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTER ESTICS:
TITLE OF INVENTION: THE IMMUNO-SUPPRES TITLE OF INVENTION: ANTIBODIES NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS: ADDRESSEE: ARNOId, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Texas COUNTRY: U.S. ZIP: 77210
                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 94.3%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-557-050-4
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Mili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-444-644-44
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APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: WAGNET, Richard W.
REGISTRATION NUMBER: 34,480
REPERBENGE/DOCKET NUMBER: 34,480
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERNCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-232-246A-21
; Sequence 21, Application US/08232246A
Patent No. 6329508
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.6°
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/08444644

Patent No. 601555

GENERAL INFORMATION: Phillip M.

TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

TITLE OF INVENTION: CONUCATES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUT TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1980
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 861-6240
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.3
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-232-246A-44
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US-08-444-644-21
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4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                         APPLICANT: Friden, Phillip M.

TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STABLE: MA.
                                                               Gaps
                                                               .;
0
Score 523; DB 3; Length 110;
Pred. No. 9.5e-54;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                   65 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                     64 OFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATION
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/23,246A
FLING DATE: 05/MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800/05077
FILING APPLICATION NUMBER: US 07/404,089
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTONENEY/AGENT INFORMATION:
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Query Match
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                                                                                                                                                                                                                                                                                                                                      5 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
                                                                                                                                                                                                                                                       Gaps
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Pred. No. 9.5e-54;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                         OYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : DB 2; Length 105;
1.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIPE 94080
ZIPE 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/23,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION DATA: 3.0
PRIOR APPLICATION DATA: 3.0
PRIOR APPLICATION DATA: 3.0
PRIOR APPLICATION DATA: 3.0
PRIOR APPLICATION DATA: 3.0
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA: 3.0
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 522; DB
Pred. No. 1.2e-
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: 1gE Antagonists
WUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P0718P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-232-539D-60
; Sequence 60, Application US/08232539D
Patent No. 5965709
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REPERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1 DNA way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0%;
92.3%;
                                                                                                                                                                                                           Query Match
Best Local Similarity 90.6%;
Matches 96; Conservative
                                                  LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: 1ines
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.3
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                      MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , TOPOLOGY:
US-08-232-539D-60
                                                                                                                                                                    US-08-232-246A-21
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6 GPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF

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63
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                                                                                                                                                                                                                                                                                                          Phillip M.
TRANSFERIN RECEPTOR SPECIFIC
ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE
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                                                                       66 NSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                     61 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 104
                                                                                                                                                                                                                                                                                                     APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR ITTLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESSE:
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.6%; Score 514; DB 3; 90.6%; Pred. No. 1.1e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-9540
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  Sequence 38, Application US/08444644 Patent No. 6015555 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Florest
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOR/We
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wagner, Richard W. REGISTRATION NUMBER: 34,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 amino acids
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Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
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Patent No. 6322508
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 88.6%; Score 514; DB 3; Length 110; Best Local Similarity 90.6%; Pred. No. 1.1e-52; Matches 96; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                      ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE FOCKET NUMBER: ALK88-15AAA
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 07/800,458
FILING DATE: 26.NOV-1991
PRIOR APPLICATION DATA.

APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: CAPPLICATION NUMBER: 07-SEP-1990
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                       USA
US-08-232-246A-38
                                                                                                                                                                                                                                                                                                              STATE: M. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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RESULT 12
US-08-569-147-85
; Sequence 85, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES

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ADDRESSER: No. 618017715, LLP
ADDRESSER: No. 6181037715, LLP
CONTENT: No. 6181037715, LLP
CONTENT: No. 6181037715, LLP
ADDRESSER: OR 6181037715, LLP
CONTENT: No. 6181037715, LLP
ADDRESSER: OR 6181037715, LLP
ADDRESSER: OR 6181037715, LLP
ADDRESSER: OR 6181037715, LLP
ADDRESSER: OR 6181037715, LLP
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ADDRESSER: OR 61810377104, LLP
ADDRESSER: OR 6181037704, LLP
ADDRESSER: OR 6181037704, LLP
ADDRESSER: OR 6181037704, LLP
ADDRESSER: OR 6181037704, LLP
ADDRESSER: OR 618103704, LLP
ADDRESSER: OR 61
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1 GVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 NSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

27.2%; Score 158; DB 3;
Best Local Similarity 35.0%; Pred. No. 6.5e-11;
Matches 36; Conservative 21; Mismatches 44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 29.7%; Score 172.5; DB 3
Best Local Similarity 35.0%; Pred. No. 1.2e-12.
Matches 36; Conservative 22; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR RILING DATE: 1995-03-15
PRIOR RILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
                                                                                                                                                                                                                                                                                                                                     P0718P3
                                                               FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA: 08/178583
FILING DATE: 07-JAN-1994
PRIOR DATE: 07-JAN-1994
PRIOR APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
APPLICATION NUMBER: 07/74768
FILING DATE: 14-AUG-1991
ATTONNEY AGENT INFORMATION: NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 90718P3
TELECOMMUNICATION INFORMATION: TELEFRAN: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08466163B
Patent No. 6329509
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 106 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-232-539D-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-08-466-163B-1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.2%; Score 175; DB 4; Length 107; 35.3%; Pred. No. 6.4e-13; tive 22; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 NSTFRVVSVLTVVHODWLNGKEYKCKVSNKGLPSSIEKTISK 107
                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc feature
LOCATION: (500)..(500)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                  NAME/KEY: misc feature
LOCATION: (451)..(451)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (530)..(530)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1382)..(1382)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:

NAME/KEY: misc_feature

LOCATION: (1812)..(1812)

OTHER INPORMATION: "n" stands for any nucleic acid
US-09-281-760E-36
ION: (413)..(414)
INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                       LOCATION: (460)..(462)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (847)..(849)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (853)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54, Application US/08212539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: 1gE Antagonists
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Conservative
                                                                                                                                        FEATURE:
NAME/KEY: misc feature
LOCATION: (460)..(462)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature LOCATION: (847)..(849)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 36; Conserva
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US-08-232-539D-54
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Search completed: November 17, 2005, 07:53:55 Job time: 23.3927 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           580
1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKTK 109
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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                                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1867879 seqs, 418409474 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                 November 17, 2005, 07:47:15
                                                                                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-674-857-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
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					COMMERTES	
Result No.	Score	& Query Match	% Query Match Length DB	DB	ΙD	Description
	572	98.6	109	18	US-10-959-318-2	Sequence 2, Appli
7	564	97.2	109	18	US-10-959-318-17	Sequence 17, Appl
٣	564	97.2	109	18	US-10-959-318-18	Sequence 18, Appl
4	554	95.5	109	18	US-10-959-318-11	17
2	554	95.5	109	18	US-10-959-318-12	Sequence 12, Appl
9	543.5	93.7	110	18	US-10-959-318-9	6
7	543.5	93.7	110	18	US-10-959-318-10	2
80	540	93.1	109	18	US-10-959-318-15	Sequence 15, Appl
С	540	93.1	109	18	US-10-959-318-16	91
10	538.5	92.8	110	20	US-11-018-102-25	25,
11	536	92.4	109	14	US-10-267-286A-4	
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1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDFEVQFNWYVDGVEVHNAKTKP 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP

REEQPNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109

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14241 6. C #9.241 9.1 9.20 9.20 9.20 9.20 9.20 9.20 9.20 9.20	Gарв
Sequence 2 Sequence 2 Sequence 2 Sequence 3 Sequence 3 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 3 Sequence 3 Sequence 2 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 5	Length 109; Indels 0; C
ng modified	B 18; e-48; .
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12 536 92.4 110 18 14 536 92.4 110 18 15 529.5 91.3 110 18 16 529.5 91.3 110 18 18 529 91.2 110 18 19 529 91.2 110 18 20 528 91.0 109 18 21 525 90.6 110 20 22 523 90.2 110 18 24 523 90.2 110 18 25 523 90.2 110 18 26 523 90.2 110 18 27 522 90.0 102 18 28 522 90.0 102 18 29 522 90.0 102 18 31 521 89.8 110 18 32 518 89.3 110 18 34 518 89.3 110 18 35 518 89.3 110 18 36 518 89.3 110 18 37 518 89.3 110 18 38 518 89.3 110 18 39 515 88.8 110 18 31 518 89.3 110 18 32 518 89.3 110 18 34 518 89.3 110 18 35 518 89.3 110 18 36 518 89.3 110 18 37 518 89.3 110 18 38 518 89.3 110 18 39 515 88.8 110 18 31 518 89.3 110 18 32 518 89.3 110 18 34 518 88.8 110 18 35 518 89.3 110 18 36 518 89.3 110 18 37 518 89.3 110 18 38 518 89.3 110 18 39 515 88.8 110 18 31 518 89.3 110 18 32 518 89.3 110 18 34 518 88.8 110 18 35 518 89.3 110 18 36 518 89.3 110 18 37 518 89.3 110 18 38 518 89.3 110 18 38 518 89.3 110 18 39 515 88.8 110 18 31 518 89.3 110 18 31 518 89.3 110 18 32 518 89.3 110 18 34 518 89.3 110 18 35 518 89.3 110 18 36 518 89.3 110 18 37 518 89.3 110 18 38 518 89.3 110 18 39 518 89.3 110 18 30 518 89.3 110 18 31 518 89.3 110 18 31 518 89.3 110 18 31 518 89.3 110 18 31 518 89.3 110 18 31 518 89.3 110 18 32 518 89.3 110 18 33 518 89.3 110 18 34 518 89.3 110 18 35 518 89.3 110 18 36 518 89.3 110 18 37 518 89.3 110 18 38 518 89.3 110 18 38 518 89.3 110 18 38 518 89.3 110 18 38 518 89	atch Sal
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OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268) OTHER INFORMATION: mutations
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Publication No. US20050215768A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Clark, Michael R
TITLE OF INVENTION:
FILE REFERENCE: 39-302
CURRENT PELING DATE: 2004-10-07
FILE REFERENCE: 2004-10-07
PRIOR PILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-10-17
PRIOR FILING DATE: 2003-10-17
PRIOR FILING DATE: 2003-10-17
SOFTWARE: Patentin version 3.3
SQ ID NOS: 27
SQ ID NO 12
LEMOTH: 109
TYPE: PRI
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APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-30
CURRENT PEDLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
SEQ ID NO 11
LENGTH: 109
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                                      61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
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Pred. No. 9.2e-47;
4; Mismatches 2;
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Pred. No. 9.2e-47;
4; Mismatches 2;
                                                                                                                                                                                                                                Sequence 11, Application US/10959318 Publication No. US20050215768A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 94.5%;
Matches 103; Conservative
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Best Local Similarity 94.5%;
Matches 103; Conservative
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COTHER INFORMATION:
US-10-959-318-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-959-318-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Variant of Human IgG2 CH2 sequence with delta d (D268) mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Variant of Human IgG2 CH2 sequence with delta e (E268) mutation US-10-959-318-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 60
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                                                                                                            Sequence 17, Application US/10959318

Publication No. US20050215768A1

Publication No. US20050215768A1

GENERAL INFORMATION:
APPLICANT: Armour, Kathryn L

APPLICANT: Clark, Michael R

ITLE OF INVENTION: POlypeptides including modified constant regions
FILE REFERENCE: 39-302

CURRENT APPLICATION NUMBER: US/10/959,318

CURRENT FILING DATE: 2004-10-07

PRIOR PILING DATE: 2004-10-07

PRIOR PILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-17

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.3
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US-10-959-318-18
i Sequence 18, Application US/10959318
j Publication No. US20050215768A1
j GENERAL INFORMATION:
j APPLICANT: Armour, Kathryn L
j APPLICANT: Clark, Michael R
j TITLE OF INVENTYON: POlypeptides including modified constant regions
j CURRENT APPLICATION NUMBER: US/10/959,318
j CURRENT FILING DATE: 2004-10-07
j PRIOR FILING DATE: 2004-10-07
j PRIOR PLILING DATE: 2003-10-17
j NUMBER OF SEQ ID NOS: 27
j SOFTWARE: PatentIn version 3.3
j SEQ ID NO 18
j LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
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Pred. No. 9.6e-48;
1; Mismatches 2;
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Best Local Similarity 97.2%;
Matches 106; Conservative
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ORGANISM: Artificial Sequence
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LENGTH: 109
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OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta b and d (D268) OTHER INFORMATION: mutations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15. Application US/10959318

| Sequence 15. Application US/10959318
| Publication No. US20050215768A1
| GENERAL INFORMATION:
| APPLICANT: Armour. Kathryn L
| APPLICANT: Clark, Michael R
| TITLE OF INVENTION: Polypeptides including modified constant regions
| FILE REFERENCE: 39-302
| CURRENT APPLICATION NUMBER: US/10/959,318
| CURRENT APPLICATION NUMBER: PCT/GB2004/004254
| PRIOR FILING DATE: 2004-10-07
| PRIOR PILING DATE: 2003-10-17
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: PatentIn version 3.3
| SEQ ID NO 15
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APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-30.
CURRENT PLING DATE: 2004-10-07
FRIOR APPLICATION NUMBER: PC7/GB2004/004254
PRIOR PLING DATE: 2004-10-07
PRIOR PLING DATE: 2003-10-17
PRIOR PLING DATE: 2003-10-17
SPIOR FILING DATE: 2003-10-17
                                                                                                                                                                     1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK
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                                                                                                            Gaps
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                                          Score 543.5; DB 18; Length 110;
Pred. No. 1e-45;
4; Mismatches 2; Indels 1;
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Publication No. US20050215768A1
GENERAL INFORMATION:
                                                   93.7%;
93.6%;
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                                                   Query Match 93.73
Best Local Similarity 93.63
Matches 103; Conservative
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Matches 100; Conservative
US-10-959-318-10
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OTHER INFORMATION: mutations
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OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, c and e (E268)
OTHER INFORMATION: mutations
                           1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                           1 APPVAGPSVFLFPPKPKPKDTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/10959318
Sequence 9, Application US/10959318
Publication No. US2005021576841
GENERAL INFORMATION:
APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including medified constant regions
FILE REFERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
FRIOR APPLICATION NUMBER: PCT/GB2004/004254
FRIOR APPLICATION NUMBER: GB324368.0
FRIOR FILING DATE: 2004-10-07
FRIOR FILING DATE: 2004-10-07
FRIOR FILING DATE: 2004-10-07
FRIOR FILING DATE: 2003-10-17
FRIOR FILING DATE: 2003-10-17
SOUTHARE PACHALIN Version 3.3
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US-10-959-318-10
| Sequence 10. Application US/10959318
| Sequence 10. Application US/10959318
| Publication No. US20050215768A1
| GENERAL INFORMATION:
| APPLICANT: Clark, Michael R
| TITLE OF INVENTY DE1yPeptides including modified constant regions FILE REFRENCE: 39-302
| CURRENT APPLICATION NUMBER: US/10/959,318
| CURRENT FILING DATE: 2004-10-07
| PRIOR FILING DATE: 2004-10-07
| PRIOR FILING DATE: 2003-10-17
| NUMBER OF SEQ ID NOS: 27
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 10
| LENGTH: 110
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Pred. No. 1e-45;
4; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 93.6%;
Matches 103; Conservative
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ORGANISM: Artificial Sequence
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US-10-959-318-21
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US-10-959-318-4
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                                     OTHER INFORMATION: Variant of Human 1gG1 CH2 sequence with delta b and e (E268) OTHER INFORMATION: mutations
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Publication No. US20030108548A1

GENERAL INFORMATION:
APPLICANT: BLUESTONE, JEFFREY A.
APPLICANT: JINDA N.
TITLE OF INVENTION: MATHODES AND MATERIALS FOR MODULATION OF THE
TITLE OF INVENTION: MATHODES AND MATERIALS FOR MODULATION OF THE
TITLE OF INVENTION: MATHODES
FILE REFERENCE: TOLT:004USC1
CURRENT APPLICATION NUMBER: US/10/267,286A
CURRENT FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: OF/557,050
PRIOR PEPLICATION NUMBER: PCT/US94/06198
PRIOR PEPLICATION NUMBER: PCT/US94/06198
PRIOR FILING DATE: 1994-06-01
PRIOR FILING DATE: 1993-06-01
PRIOR FILING DATE: 1993-06-01
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Publication No. US20050136061A1
GENERAL INFORMATION:
APPLICANT: Centocor, Inc.
TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN5045 USA NP
CURRENT APPLICATION NUMBER: US/11/018,102
CURRENT FILING DATE: 2004-12-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                   1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTKP
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92.8%; Score 538.5; DB 20; Length 110;
Best Local Similarity 93.6%; Pred. No. 3.1e-45;
Matches 103; Conservative 2; Mismatches 4; Indels 1;
                                                                                                                                    Length 109;
                                                                                                                                                                                 4; Indels
                                                                                                                                 Query Match
93.1%; Score 540; DB 18;
Best Local Similarity 91.7%; Pred. No. 2.2e-45;
Matches 100; Conservative 5; Mismatches 4;
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                    US-10-959-318-16
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US-10-267-286A-4
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LENGTH: 110
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Fublication No. US20050215768A1
GENERAL INFORMATION:
APPLICANT: Armour. Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39.302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-10-17
PRIOR FILING DATE: 2003-10-17
SRIOR FILING DATE: 2003-10-17
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
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                                                                                                                                                                                                                                                                           Length 109;
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Pred. No. 5.5e-45;
3; Mismatches 3;
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Publication No. US20050215768A1
GENERAL INFORMATION:
APPLICANT: ATMOUR, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including mod
FILE REPERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION WUMBER: PCT/GB2004/004254
PRIOR FILING DATE: 2004-10-07
                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                      Query Match 92.4%;
Best Local Similarity 94.3%;
Matches 100; Conservative
NUMBER OF SEQ ID NOS: 23
SOFTWARR: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 109
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Best Local Similarity 94.33
Matches 100; Conservative
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ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268)
OTHER INFORMATION: mutations
US-10-959-318-13
                                                                                                                                                                                                                                                                                                        53
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Best Local Similarity 90.99
Matches 100; Conservative
  ; SEQ ID NO 13
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Job time
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                                                                                                                                                                                                       OTHER INFORMATION: Variant of Human 1gG4 CH2 sequence with delta e (E268) mutation
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TITLE OF INVENTION: ANTI-EETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
TITLE OF INVENTION: ANTI-EETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
CURRENT APPLICATION NUMBER: US/11/018,102
CURRENT FILING DATE: 2004-12-21
SUPPRESS OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.3
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US-10-959-318-13
i Sequence 13, Application US/10959318
i Sequence 13, Application No. US20050215768A1
i GENERAL INFORMATION:
i APPLICANT: Armour, Kathryn L
i APPLICANT: Clark, Michael R
i TITLE OF INVENTION: POLYPEPTIGES including modified constant regions
FILE REFERENCE: 39-302
i CURRENT APPLICATION NUMBER: US/10/959,318
i CURRENT APPLICATION NUMBER: US/10/959,318
i PRIOR PLILING DATE: 2004-10-07
i PRIOR FILING DATE: 2004-10-07
i PRIOR FILING DATE: 2003-10-17
i NUMBER OF SEQ ID NOS: 27
i SOFTWARE: Patentin version 3.3
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Pred. No. 5.5e-45;
3; Mismatches 3;
PRIOR APPLICATION NUMBER: GB0324368.0 PRIOR FILING DATE: 2003-10-17 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.3 SEQ ID NO 21 LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 24, Application US/11018102; Publication No. US20050136061A1; GENERAL INFORMATION:
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Best Local Similarity 94.3
Matches 100; Conservative
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US-11-018-102-24
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November 17, 2005, 06:38:35; Search time 91.6667 Seconds (without alignments) 464.112 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                            OM protein - protein search, using sw model
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US-09-674-857-3 Perfect score: Title:

1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110 BLOSUM62 Sequence:

2105692 segs, 386760381 residues Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2003as:*
7: geneseqp2003as:*
8: geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Mutated C	Mutated C	コ	HuEPO-L-v	Human GCS		Human FGF	Human FGF	Human FGF	MoTAbii f	Human AQC	Human imm	Human mut	Human mut	Human mod	Modified	Modified	Amino aci	Human mod	Human imm	Ztnfr12-t	Human TAC	Human TAC	Himan TAC
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ID	AAY54998	AAY54996	ADM33857	ADR48988	ADM33380	AAW85689	AAY97175	AAY97174	AAY97173	AAW85692	AAE33524	AAE35231	ABB81492	ABB81491	AAE35220	AAY05688	AAW97756	AAB07541	AAE35218	AAE35219	ABB81493	AAE35228	AAE35224	AAR35225
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% Query Match	98.1	97.2	7	7	97.1	95.7	95.7	95.7	95.7	95.7	92.6	95.4	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	6,0
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AAE35223 ADM33855 ADR48986 ADM33378	ABB81645 ADF83613 AAU76912 AAE30845	AAU76916 AAE30844 ABR83693	AAB85286 ABG67217 AAE23361	AAE29072 AAB85274 AAU04062 ABG67205
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ALIGNMENTS

RESULT 1

Binding molecule; CH2 sequence; complement dependent lysis; FogammaRIIb; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-ve-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopaenia; arthitis; erythroblastosis focealis; neonatal alloimmune thrombocytopaenia; Goodpastures disease; therapy; sickle cell anaemia; coronary artery occlusion. (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD. Williamson LM; AAY54998 standard; protein; 110 AA Mutated CH2 sequence Gldeltaac. 99WO-GB001441. 98GB-00009951. 17-FEB-2000 (first entry) Clark MR, 07-MAY-1999; 08-MAY-1998; W09958572-A1 18-NOV-1999. Armour KL, Synthetic. AAY54998; AAY54998

WPI; 2000-039075/03.

Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties.

Claim 12; Fig 17; 81pp; English.

and This sequence represents the mutated CH2 molecule Gldeltaac, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; a (b) an effector domain that is homologous to all or part of a constant

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domain of a human immunoglobulin G (IgG) heavy chain. The binding molecule is used to bind a target molecule (especially FogammaRID causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule is useful for the tradement of graft-venolection, autoimmunity (e.g. an antibody, to the target cattoimmune thrombocytopaenia and arthritis, autoimmune thrombocytopaenia and arthritis), alloimmunity (e.g. cattoimmune thrombocytopaenia and arthritis), alloimmunity (e.g. cattoimmune thrombocytopaenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN chronic or acute inflammatory diseases (e.g. Crohn's, HDN coronary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FogammaR and desirable thoman amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent with being able to cross the human placenta through interaction with FCRn consistent.
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99.1%; Pred. No. 1.4e-51;
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Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 110 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin

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This sequence represents the mutated CH2 molecule Gldeltaab, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without tringgering complement capable of binding domain capable of binding a target molecule; and dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (CD) an effector domain that is homologous to all or part of a constant comman in mimunoglobulin G (IgG) heavy chain. The binding causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule is useful for the treatment of graft-vs. The binding molecule is useful for the treatment of graft-vs. Compaction, autoimmunity (e.g. vasculitis, autoimmune harmonlytic anaemia, autoimmune thrombocytopaenia and arthritis), alloimmunity (e.g. autoimmune thrombocytopaenia and arthritis), alloimmunity (e.g. chronic or acute inflammatory diseases (e.g. Crohn's, HDN contarl inflammatory diseases (e.g. Crohn's, HDN compactions and arthritis and activate complement or tringger cytotoxic activities through FogammaR and desirable complement or tringger cytotoxic activities through FogammaR and desirable thuman amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent immunogenically consistent through interaction with FCRn consistent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APPVA-GPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erythropoietin; EPO; immunoglobulin; IgG; fragment crystallisation region; Fc; chronic anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis; AIDS; myelodysplastic syndrome; (HuEFO)-L-vFcgammal; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.2%; Score 570.5; DB 3; Length 109; 99.1%; Pred. No. 5.3e-51; ive 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .27
note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human HuEPO-L-vFcgammal fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM33857 standard; protein; 435 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein 209. .435
/note= "IgG1 Fc"
Misc-difference 222
                                                                Claim 12; Fig 17; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "EPO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "b.
7.208
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Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 109 AA;
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properties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
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The invention relates to a recombinant human erythropoietin (Hubbo)-L-vFC fusion protein comprising HubFO, a peptide linker, and a human C fragment crystallisation reegion) variant. Also included is a carbohydrate-derived cell line producing the human crospension by the cases of 10 midrogramme per million cells in a 24-hour period. The HubFO L-vFC fusion protein cited above in its growth medium in crospaneme per million cells in a 24-hour period. The HubFO L-vFC fusion protein exhibits an enhanced in vitro biological activity of at least 2-fold relative to that of recombinant HubFO on a molar of at least 2-fold relative to that of recombinant HubFO on a molar contains amino acid mutations to attenuate effector functions. The lugger contains amino acid mutations to attenuate effector functions. The human comprises a hinge, CH2 and CH3 domains of human igG2 with pro331Ser mutations, human igG4 with Ser228Pro and Leu235Ala mutations, or human igG1 with Leu234Val, Leu235Ala and Pro331Ser mutations, or human igG1 with chronic anaemia caused by renal failure, cancer crecombinant human erythropoietin-L-vFc fusion protein in frequent injections to myelodysplastic syndrome. The increased activity and prosoned prosoned presence of the human erythropoietin-L-vFc fusion protein in the serum, as compared to prior art, leads to lower dosages and less frequent injections result in better patient compaliance and quality, and less frequent injections result in better patient compaliance and quality of life. The present sequence represents the fusion protein HuEPO-L-vFcgammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant human erythropoietin-L-vFc fusion proteins, useful for treating patients with chronic anemia caused by renal failure, cancer chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
/note= "Wild-type Leu substituted by Val"
                                                                                 /note= "Wild-type Leu substituted by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 2C; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                               17-AUG-2001; 2001US-00932812
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-2001; 2001US-00932812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sun LK, Sun BNC, Sun CRY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003-616080/58.
                                           Misc-difference 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUN L K.
SUN B N C.
SUN C R Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADM33856
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                                                                                                                                                                                  US2003082749-A1
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                                                            1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                 Gaps
                                                                                                                       61 PREEQYNSTYRVVSVLTVIHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                       219 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 328
                              Indels
97.1%; Score 570; DB 7;
97.3%; Pred. No. 3.2e-50;
iive 1; Mismatches 2
                               Conservative
            Local Similarity
nes 107; Conserv
                   Best Loca
Matches
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Length 435;

Query Match

RXB

ADR48988 standard; protein; 435 AA. ADR48988 ADR48988

HuBPO-L-vFc fusion protein #2.

antianaemic; nephrotropic; human; HuBPO-L-vPc; erythropoietin; EPO; anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis; AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.

Homo sapiens. Synthetic.

US2004175824-A1

09-SEP-2004.

21-JAN-2004; 2004US-00761593

17-AUG-2001; 2001US-00932812

(SUNL/) SUN L K. (SUNB/) SUN B N C. (SUNC/) SUN C R Y.

Sun CRY; Sun BNC, Sun LK,

2004-634851/61. N-PSDB; ADR48987 New recombinant HuEPO-L-vPc fusion protein comprises human erythropoietin (HuEPO), a peptide linker, and a human IgG Pc variant, useful for treating chronic anemia due to renal diseases, cancer chemotherapy, or rheumatoid arthritis.

Claim 5; SEQ ID NO 22; 31pp; English.

N-PSDB; ADM33379

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protein is useful for treating patients with chronic anemia due to renal diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for HIV infection, or myelodysplastic syndrome. It is also useful in the treatment of renal failure. A fusion protein was assembled from several DNA segments. To obtain the gene encoding the leader peptide and mature protein of human erythropotetin (EPO), cDNA library of human fetal liver or kidney was used as the template in polymerase chain reaction (PCR). For the convenience of cloning, SEQ ID NO. 1 which incorporates a restriction enzyme cleavage site is used as the S. Oligonucleotide primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon and incorporates a BamHI site. The resulting DNA fragments of approximately GOD by were inserted into a holding vector such as pUCI9 at the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the human EPO gene was confirmed by DNA sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 435 AA;
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                                                                                      219 APEVAGGPSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278
                                                                     9
                                                                 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                    Gaps
                                                                                                                                     PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                      PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 328
                                    ;
0
   Length 435;
                                    2; Indels
 Score 570; DB 8;
Pred. No. 3.2e-50;
                                1; Mismatches
   97.18;
97.38;
Query Match
Best Local Similarity 97.3
Matches 107; Conservative
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ADM33380 standard; protein; 447 AA ADM33380 RESULT

ADM33380;

(first entry)

03-JUN-2004

Human GCSF-L-fragment of crystallisation gamma 1 fusion protein.

cytostatic; immunostimulant; antianaemic; anti-HIV; protein therapy; human; granulocyte colony-stimulating factor; GCSF; GCSF-L-vFc; immunoglobulin G; IgG; fragment of crystallisation; immune disorder; haematopoietic disorder; cancer; chemotherapy; leukaemia; anaemia; AIDS; bone marrow transplantation; chronic neutropenia; fusion protein; fragment of crystallisation gamma 1; Fc gamma 1.

Homo sapiens Synthetic

note= "Wild type Leu substituted by Val" 'note= "Wild type Leu substituted by Ala" Location/Qualifiers Misc-difference Misc-difference Misc-difference

/note= "Wild type Pro substituted by

US2003082679-A1

01-OCT-2001; 2001US-00968362

01-OCT-2001; 2001US-00968362

SUN L K.
SUN B N C.
SUN C R Y. (SUNL/) (SUNC/)

Sun BNC, Sun LK, WPI; 2003-585400/55.

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The invention describes a recombinant human granulocyte colony-
stimulating factor (NG-CSF)-L-vFc fusion protein comprising NG-CSF, a
peptide linker, and a human immunoglobulin G (IGG) Fc variant. Also
described are: a CHO-derived cell line producing the above NG-CSF-L-vFc
fusion protein in its growth medium in excess of 10 kmgr;g per million
cells in a 24-hour period; and making the recombinant fusion protein
cited above, comprising generating a CHO-derived cell line cited above,
growing the cell line under conditions the recombinant fusion protein is
expressed in its growth medium, and purifying the expressed protein. The
recombinant fusion protein is useful in treating a variety of conditions
associated with an impaired immune or haematopoietic system, including
cancer chemotherapy. Jeukaemias, anaemias, AlDS, bone marrow
cransplantation, and chronic neutropenias. This is the amino acid
sequence of human GCSF-L-fragment of crystallisation gamma 1 variant
                                                                               vFc fusion protein for treating immune or hematopoietic system disorders comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin
                                                   New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-
                                                                                                                                                                                         Disclosure, Fig 2C; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fusion protein.
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Sequence 447 AA;

Gaps . 0 Score 570; DB 7; Length 447; Pred. No. 3.3e-50; 1; Mismatches 2; Indels 97.1%; 97.3%; Best Local Similarity 97.3 Matches 107; Conservative Query Match

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231 APEVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 290 9 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 셤 ò

RESULT 6 AAW85689

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AAW85689;

AAW85689 standard; protein; 468

(first entry) 12-AUG-1999

D9D10 heavy chain fusion protein.

interferon gamma; IFN; treatment; prevention; septic shock; cachexia; immune disease; multiple sclerosis; Crohn's disease; skin disorders; inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv; multivalent; ruminant. Antibody; humanised; variable region; heavy chain; light chain;

Synthetic. Mus musculus

Location/Qualifiers Peptide Key

/note= "Humanised heavy chain variable domain of D9D10" /note= "D9D10 light chain signal peptide" .137 Domain

138. .467 /note= "Human IgG1 heavy chain constant domain" Misc-difference 468

Domain

/note= "Leu added by cloning strategy"

WO9909055-A2

25-FEB-1999

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Human FGF-RI Extracellular domain-Ig Fc fusion protein 6.
      04-DEC-2000 (first entry)
    New antibodies which bind and neutralise interferon-gamma (IFN gamma) can be used as a medicant, for preventing or treating septic shock, cachexia, immune diseases including multiple solerosis and Crohn's disease and skin disorders including bullous, inflammatory and neoplastic dermatoses. The disorders including bullous, inflammatory and neoplastic dermatoses. The antibody is selected from a single chain antibody (scFv), a chimeric antibody of diabody comprising the humanised variable domain of the monoclonal mouse anti-IFN gamma antibody bDB10; a multivalent antibody; (scFv) and sample. Two fusion CDB10; a multivalent antibody; (scFv) as sample. Two fusion CDB10; a multivalent antibody; (scFv) as sample. Two fusion CDB10; a multivalent antibody; (scFv) as sample. Two fusion CDB10; a multivalent antibody; (scFv) as sample. Two fusion CDB10; a multivalent antibody; (scFv) as sample. Two fusion CDB10; a multivalent antibody; (scFv) as sample. Two fusion CDB10; a multivalent antibody; (scFv) as sample. Two fusion CDB10; a multivalent antibody; (scFv) as sample. Two fusion constant domain in which the Clq-complement binding site comparised CDB10 heavy chain constant domain in which the Clq-complement binding site (and the subsequently amplified using two primers (AAX08589, AAX08589) to generate PCR-VI fragment. The two primers (AAX08599, AAX08599) to generate PCR-VI fragment. The two fragments had a base pair overlap and were muplified with two primers (AAX08599, AAX08599, AAX08599, CC give pGBM-T to give pGBM-T-Wh using two primers (AAX08599, AAX08599, AAX08599, AAX08599, AAX08599, AAX08599, AAX08599, AAX08599, AAX08500 and the resulting PCR-X fragment inserted into pGBM-T CC generate PCR-VII fragment and AAX08599, AAX08599, AAX08599, AAX08500 and the resulting PCR-X fragment inserted into pGBM-T complement compared the overlapped and fused using primers (AAX08599, AAX08599, AAX08599, AAX08500 and the resulting PCR-X fragment inserted into pGBM-T compared the overlapped and fused using prompared into compared the
                                                                                                                                                                               New engineered antibodies which bind and neutralise interferon-gamma -
useful for prevention and treatment of septic shock, cachexia, immune
diseases and skin disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEMHD9D10H. For a description of the construction of the light chain tusion cDNA see GENESEQ records AAX08573-X08584
                                                                                                                                                                                                                                           Disclosure; Fig 9; 134pp; English.
                             97EP-00870122.
98EP-00870139.
 98WO-EP005165
                                                                         (INNO-) INNOGENETICS NV.
                                                                                                                                   WPI; 1999-180969/15.
N-PSDB; AAX08631.
                                                                                                       Sablon E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 468 AA;
14-AUG-1998;
                            18-AUG-1997;
18-JUN-1998;
                                                                                                       Buyse M,
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1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60 Gaps ö 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 360 95.7%; Score 562; DB 2; Length 468; 95.5%; Pred. No. 2.4e-49; ive 2; Mismatches 3; Indels Conservative Similarity Matches 105; 311 Query Match Local g ò 셤

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AAY97175 standard; protein; 488 AA AAY97175; AAY97175 ID AAY9 XX AC AAY9

RESULT

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FGF-R; fibroblast growth factor receptor; extracellular domain; IgGl; immunoglbbulin; Gl; oligomerization domain; Fc region; fusion protein; inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary; ophthalmological; anti-proliferative
                                                                                                                                                                                                                                                                                                                                                                                                          /label= L276E
/note= "This mutation decreases the affinity of the Fc
portion for Fc receptors"
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                                                                                                                                                                                                                                                                                                                                                  /label= Human_IgG1_Fc_region
/note= "Contains hinge region and domains CH2 and CH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "This mutation decreases the affinity of the portion for complement"
                                                                                                                                                                                    l. .21
/label= FGF-R1_signal_peptide
                                                                                                                                                                                                                                                                                                              'label= Ig_III_segment
                                                                                                                                                                                                                                                                  Ig_II_segment
                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= P376S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-2000; 2000WO-US003166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0119002P
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                                                                                                                                                                                                                                                                                            . 222
                                                                                                                                                                                                                                                                                                                                  .488
                                                                                                                                                                                                                                                                    /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA52132.
                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200046380-A2
                                                                                                  Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-1999;
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                                                                                                                                                        Peptide
                                                                                                                                                                                              Domain
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                                                                                                                                                                                                                                                                                                                                  Region
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New polypeptide comprising a fibroblast growth factor receptor extracellular domain fused to a heterologous oligomerization domain for treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.

Claim 14; Page 68-69; 70pp; English.

Novel fusion protein constructs comprise a fibroblast growth factor (FGF) receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin (Ig) I segment fused to a heterologous oligomerization domain that comprises an immunoglobulin Fc region, HIV, CH2, CH3 or CH4 region, or light chain of an immunoglobulin molecule, or a peptide with a recinc ripper motif. The Ig1 segment is not necessary for binding of acidic FGF and basic FGF (BFGF). The Ig1 deletion further increases the acidic FGF and heparin, protects the core of the molecule from affinity for aFGF and heparin, protects the core of the molecule from proteclysis, and abrogates the heparin requirement for aFGF-R monomer proteins. The FGFR-IG FC fusion dimers are active as FGF-R monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The fusion constructs are useful to treat FGF- angiogenesis. or FGF-Rs. The fusion constructs are useful to treat FGF-, angiogenesis. or FGF-Rs. Cectal, testis and cervical tumours), neovascularization (e.g. bladder, breast, lung, rectal, testis and cervical tumours), neovascularization (e.g. diabetic retinogathy, neovascular glaucoma, wound healing and corneal scarring) postangioplasty and postatherectomy restenosis)

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Novel fusion protein constructs comprise a fibroblast growth factor (FGF)

receptor (FGF-R) extracellular domain (BCD) lacking the immunoglobulin

(Ig) I segment fused to a heterologous oligomerization domain that

comprises an immunoglobulin For region, CH1, CH2, CH3 or CH4

comprises an immunoglobulin molecule, or a peptide with a

region, or light chain of an immunoglobulin molecule, or a peptide with a

leucine zipper motif. The Ig I segment is not necessary for binding of

acidic FGF and beaic FGF (FGF). The Ig I deletion further increases the

confinity for a FGF and heparin, protects the core of the molecule from

proteolysis, and abrogates the heparin requirement for aFGF binding. The

confinity for a FGF Ig FC fusion dimers are active as FGF antagonists at

proteins. The FGFR-IG FC fusion dimers are active as FGF antagonists at

conformer protein as competitors of bFGF binding to immobilized FGF-R

custom constructs are useful to treat FGF-, angiogenesis, or FGF-R

conformer protein as competitors of bFGF binding to immobilized FGF-R

cuctal, testis and cervical tumours), neovascularization (e.g. diabetic

rectal, testis and cervical tumours), neovascularization (e.g. diabetic

retinopathy, neovascular glaucoma, wound healing and corneal scarring)

and hyper-proliferation of vascular smooth muscle cells (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           extracellular domain fused to a heterologous oligomerization domain for treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region 294...525 / label= Human IgG1 Fc_region / label= Human IgG1 Fc_region / note= "Contains hinge region and domains CH2 and CH3" Misc-difference 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1; immunoglobulin; G1; oligomerization domain; Fc region; fusion protein; inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary; ophthalmological; anti-proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human FGF-RI Extracellular domain-Ig Fc fusion protein 4.
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/label= FGF-Rl_extracellular_domain
/note= "Ig I segment is deleted"
                                                                                                                                                                                                                                                                                                                                                                                                              95.7%; Score 562; DB 3; L
95.5%; Pred. No. 2.5e-49;
live 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .. .21
|label= FGF-R1_signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77. 139
/label=_ig_II_segment
                                             Claim 14; Page 65-66; 70pp; English.
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/label= Li
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/label= A
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 497 AA;
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                                                                                                                          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                 FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1; immunoglobulin; G1; oligomerization domain; Fc region; fusion protein; inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary; ophthalmological; anti-proliferative.
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/label= Linker
266. .497
/label= Human IgGl FC region
/note= "Contains hinge region and domains CH2 and CH3"
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "This mutation decreases the affinity of the portion for complement"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22. .257
/label= FGF-Rl_extracellular_domain
/note= "The Ig I segment and acid box are deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "This mutation decreases the affinity of portion for Fc receptors"
                                                                                                                                                                     PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide comprising a fibroblast growth factor receptor
                                                Length 488;
                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                     Human FGF-RI Extracellular domain-Ig Fc fusion protein 5.
                                                95.7%; Score 562; DB 3; 95.5%; Pred. No. 2.5e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .21
/label= FGF-R1_signal_peptide
                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59. .111
/label=_ig_II_segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                              AAY97174 standard; protein; 497 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= L285E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= P385S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2000; 2000WO-US003166.
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                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-514961/46.
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                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                       Seguence 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-1999;
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                                                                                                                                                                      61
                                                  Query Match
                                                                  Best Local
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fusion protein.

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receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin
(Ig) i segment fused to a heterologous oligomerization domain that
comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4
region, or light chain of an immunoglobulin molecule, or a peptide with a
clearine zipper motif. The Ig I segment is not necessary for binding of
acidic FGF and basic FGF (BFGF). The Ig I deletion further increases the
affinity for aFGF and heparin, protects the core of the molecule from
affinity for aFGF and heparin, protects the core of the molecule from
core fusion polypeptides are better FGF inhibitors than FGF-R monomer
proteins. The FGFR-IG Fc fusion dimers are active as FGF-R monomer
protein as competitors of BGFP binding to immobilized FGF-Rs.
Chusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R.
Chaic molomer protein as tumourigenesis (e.g. bladder, breast, lung,
rectal, testis and cervical tumours), neovascularization (e.g. diabetic
retinopathy, neovascular glaucoma, wound healing and corneal scarring)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                          /note= "The mutation decreases the affinity of the portion for complement" 445. .250
/label= L313E
/note= "The mutation decreases the affinity of portion for Fc receptors"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          postangioplasty and postatherectomy restenosis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 562; DB 3;
Pred. No. 2.7e-49;
2; Mismatches 3
                                                                                            /label= Ig_III_segment
                                                                                                                                                                                                                                                                                                                                                  Claim 14; Page 61-62; 70pp; English.
                                               /label= P409S
                                                                                                                                                                 07-FEB-2000; 2000WO-US003166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.7%;
95.5%;
                                                                                                                                                                                          99US-0119002P
                                                                                                                                                                                                                                        Ballinger M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 105; Conservative
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                                                                                                                                                                                                               (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 525 AA;
                                                                                                                  WO200046380-A2
                                                                                                                                                                                                                                       Kavanaugh WM,
                                                                                                                                                                                          08-FEB-1999;
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                                                                                  Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon gamma; IFN; treatment; prevention; septic shock; cachexia; immune disease; multiple sclerosis; Crohn's disease; skin disorders; inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
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                                                                                                                                                                                                                                                                                                   D9D10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New engineered antibodies which bind and neutralise interferon-gamma useful for prevention and treatment of septic shock, cachexia, immune diseases and skin disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                           /note= "Humanised heavy chain variable domain of
Antibody; humanised; variable region; heavy chain; light chain;
                                                                                                                                                                                                                                                                                                                                                'note= "Human IgG1 heavy chain constant domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                          1. .20
/label= Mouse_D9D10_light_chain_signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.7%; Score 562; DB 2; Length 71
95.5%; Pred. No. 3.9e-49;
ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                              note= "Leu added by cloning strategy"
                                                                                                                                                                                                                                                                                                                                                                                                                      469. 472
/label= Gly(3)Ser_linker
473. 711
/label= Humanised)_D9D10_ScFv
                                                                                                                                                                                                .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 20; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-EP005165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97EP-00870122,
98EP-00870139.
                                                                                                                                                                                                                                                                                                                           .467
                                                                                                                                                                                                                                                                         .137
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                                                                                                  multivalent; ruminant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-180969/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buyse M, Sablon E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAW85692,
                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 711 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9909055-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1999
                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                Key
Peptide
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                                                                                                                                                                                                                                                                         Domain
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RESULT 11

AAW85692 standard; protein; 711 AA

12-AUG-1999 (first entry)

AAW85692;

AAW85692 ID AAW8 XX AC AAW8 XX DT 12-A

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the present invention tetaces to mover antiboures that specifically Ding to very late activation (VLA-1; betal containing integrins) antigens and methods of using these antibodies to treat immunological disorders. The antibodies are useful for preventing or treating VLA-1 conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal conditions (e.g. psoriasis, respiratory distress syndrome, asthma, chronitis, tendonitis, pursitis, inspiratory distress syndrome, asthma, chronitis, tendonitis, bursitis, respiratory distress syndrome, asthma, continies, tendonitis, bursitis, prever migraine headaches, gastro-cintestial conditions (e.g. inflammatory bowel disease, Crohn's disease, conscitis and colorectal cancer), cascular diseases (e.g. inflammatory bowel disease, crohn's disease, rheumatic fever, osteoarthritis, osteomic diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid arthritis, systemic lupus erythematosus and multiple sclerosis), renal callure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, ginglitity, or immediate hypersensitivity), graft and transplant rejections, graft columnosis host disease, conjunctivitis, swelling occurring after injury, error myocardial ischaemia or endotoxin shock syndrome. The present sequence is human AQC2 heavy chain mutant protein, hsAQC2
                                                                                                                                                                                                 Human; very late activation antigen; VLA-1; betal containing integrin; immunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; arberosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis; systemic lupus erythematosus; multiple solerosis; neptrotic syndrome; renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis, eczema, burns, dermatitis, and abnormal proliferation of hair follicle cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention relates to novel antibodies that specifically bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Karpusas M;
                                                                                                                                                                 Human AQC2 heavy chain mutant protein, hsAQC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 23; Page 92; 248pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saldanha JW,
                          AAE33524 standard; protein; 447 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-APR-2001; 2001US-0283794P.
06-JUL-2001; 2001US-0303689P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2002; 2002WO-US011521
                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-093009/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOJ ) BIOGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                   02-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD,
                                                                        AAE33524;
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Score 561; DB 6; Length 447; Pred. No. 2.8e-49;

95.6**%**; 95.5**%**;

Query Match Best Local Similarity

Sequence 447 AA;

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The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or ZTNF4; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammalian subject. The composition comprising the fusion protein may also be used in treating cutoimmune diseases (e.g. systemic lupus erythematosus, multiple solerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft crejection, anaemia and septic shock. The fusion proteins are also used in group therapy. The present sequence is human immunoglobulin gammal mutant protein. This sequence is used in the exemplification of the invention. Note: This sequence is not shown in the specification, however it is
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                                                                           232 APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 291
                                   1 APPVAGGESVFLFPPKEKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin; anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive; glomerulonephrits; asthma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; human; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI)-immunoglobulin fusion protein, for treating cancer or diabetes, comprises a TACI receptor group and an immunoglobulin group.
  Gaps
                                                                                                                     61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                             ..
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                      Human immunoglobulin gammal mutant protein, Al34S.
    4;
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  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                  AAE35231 standard; protein; 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-2002; 2002WO-US015910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-2001; 2001US-0293343P
                                                                                                                                                                                                                                                                                                                                                   28-MAY-2003 (first entry)
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      Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated human tumor necrosis factor receptor polypeptide, termed Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Ztnfr12; tumour necrosis factor receptor; cytostatic; immunosuppressive; dermatological; antinflammatory; antidabetic; neuroprotective; antixheumatic; antiarthritic; antiasthmatic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthema; rheumatoid arthitis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; bronchitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; enal neoplasm; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft-versus host disease; graft rejection; Crohn's disease.
constructed based on human immunoglobulin gammal protein (SEQ ID NO:6) sequence shown in column 92-93 (AAE35214)
                                                                                                                                                                            1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                         Gaps
                                                                                                                                                                                                                           PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                            ö
                                                                                       Length 251;
                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human mutated Fc protein designated Fc5 SEQ ID NO:32.
                                                                                     95.4%; Score 560; DB 6; 95.5%; Pred. No. 1.8e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ztnfr 12, useful for treating autoimmune dis
renal failure or renal disease and lymphoma.
                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 148-149; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grant FJ;
                                                                                                                                                                                                                                                                                                                                                  ABB81492 standard; protein; 232 AA
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20-DEC-2000; 2000US-0257131P.
28-JUN-2001; 2001US-0301715P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-2001; 2001US-0315565P
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                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-508212/54.
                                                                                                     Local Similarity
tes 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Χu w,
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                                                    Sequence 251 AA;
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                                                                                                                                                                                         35
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                                                                                     Query Match
                                                                                                         Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                 RESULT 13
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lymphocytes, activated B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour cells. [1] is useful for treating autoimmume disorders such as systemic lupus erythematosus, myasthemia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, rheumatoid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid leukaemia, nephritis, and pyelonephritis, and for treating renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel disease, graft-versus host clisease, graft rejection and Crohn's disease. [1] is useful for modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody communication. Human Ztnfr12 is located to chromosome 22q13.2. The present sequence represents a mutaced Fc protein designated Fc5, which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
for treating disorders and diseases associated with B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.1%; Score 558; DB 5; Length 232; 95.5%; Pred. No. 2.6e-49; ive 0; Mismatches 5; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human mutated Fc designated Fc4 protein SEQ ID NO:28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB81491 standard; protein; 232
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2000US-0257131P.
2001US-0301715P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 95.5
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200238766-A2
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20-DEC-2000;
28-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB81491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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8X8888888888888888888888888888888
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Matches 105; Conservative
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                                                                                                                                                                                                           The present invention describes a human tumour necrosis factor receptor designated Ztnfr12 [1]. [1] has cytostatic, immunosuppressive, dermatological, antiinflammatory, neuroprotective, antidiabetic, antiarthratic, antiarthmatic, nephrotropic and hypotensive activities, and can be used in gene therapy. [1] can be used for inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12 (e.g. ZTNF4), for treating disorders and diseases associated with B (c.g. Tymphocytes, activated B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour cells. [1] is useful for treating cutoimmune disorders such as systemic lupus expthematosus, mysathenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, rheumatoid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as glomerulonephritis, vacultis, chronic lymphoid cleukaemia, nephritis, and pyelonephritis, and for treating renal cleukaemia, multiple myelonas, lymphonas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft-versus host disease, graft rejection and Crohn's disease. [1] is useful for modulating the immune system, for regulating B cell responses and development, for modulating and cytokine production, and for modulating T and B cell communication. Human Ztnfr12 is located to chromosome 22q13.2. The crommunication. Human Ztnfr12 is located to chromosome 22q13.2. The communication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                     Novel isolated human tumor necrosis factor receptor polypeptide, termed 2tnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 APEAEGAPSVFLFPPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PREEDYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 558; DB 5; Length 232;
Pred. No. 2.6e-49;
0; Mismatches 5; Indels
                                                                                                                                                                            Example 4; Page 146; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.1%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 105; Conservative
     WPI; 2002-508212/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                              N-PSDB; ABN89444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 232 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
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Human modified immunoglobulin moiety #3. AAE35220 standard; protein; 250 AA (first entry) 28-MAY-2003 AAE35220; AAE35220

g ò

Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TYCI; tumour necrosis factor-like protein; ZTNES; ZTNEY; immunoglobulin; anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive; glomerulonephritis; asthma; bronchitis; graft rejection; septic shock; glomerulonephritis; neuroprotective; cyclophilin ligand-interactor; human; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation. Homo sapiens Synthetic.

WO200294852-A2 28-NOV-2002

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The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumour necrosis factor-like protein (STNRP) 2 or ZTNP4; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammalian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus, multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft rejection, anaemia and septic shock. The fusion proteins are also used in molety used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane activator and calcium modulator and cyclophilin ligand-
interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
diabetes, comprises a TACI receptor group and an immunoglobulin group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 110-111; 71pp; English
20-MAY-2002; 2002WO-US015910
                                                                                   24-MAY-2001; 2001US-0293343P
                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                    Gross JA;
                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-148455/14.
                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD53758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 250 AA;
                                                                                                                                                                                                                                                                    Rixon MW,
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15 APEABGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94 completed: November 17, 2005, 07:04:55 ne : 92.6667 secs

Job time

9

0; Gaps

Length 250; Indels

95.1%; Score 558; DB 6; L 95.5%; Pred. No. 2.8e-49; Live 0; Mismatches 5;

Local Similarity

1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

November 17, 2005, 06:49:37; Search time 18.0822 Seconds (without alignments) 585.319 Million cell updates/sec Run on:

US-09-674-857-3 Title: Perfect score:

1 APPVAGGPSVFLFPPKFKDT......CKVSNKGLPSSIEKTISKAK 110 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	•						Ig gamma-3 chain C		gamma-3			gamma	heavy ch	gamma		gamma-2b		gamma ch										Ig gamma-1 chain C	=
SUMMARIES	OI	PT0207	S31866	СННО	869339	G4HU	G2HU	A23511	A60764	G3HUWI	147160	147159	147162	S22080	147161	147158	PS0018	C30554	GHRB	G2GP	S31459	G3MSC	G3MSM	806611	G2MSBM	G2MS11	G1MS	S00847	G1MSM	PC4436
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ф	Query Match	94	94	94	94	94	92	91	91	88	78	78	77	75	73	73	73	71	71	71	71	71	71	69	67	67	67	67	67	67
	Score	557	557	557	557	553	543.5	539	539	519	458	458	453	440	434	434	431	421	421	421	421	418	418	410	397	397	396	396	396	396
	Result No.	П	7	М	4	Ŋ	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain		Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-1 chain C	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma heavy cha	Ig epsilon-chain -	Ig epsilon chain C	Ig gamma-1 chain C	Ig heavy chain pre	Ig epsilon chain C
GZMSAB	G2MSA	G2MSAM	S374B3	501321	840295	PS0017	PS0019	B30503	A30503	146732	I36948	ЕННО	S14236	S04845	EHRT
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335 1	330	399 1	469	475	446	326	322	112	88 2	180 2	426 2	428 1	152 2	549	429
67.1 335 1															
	9.99	9.99	9.99	65.2	64.9	64.7	57.8	52.6	47.0	42.4	28.5	28.4		26.7	26.1

ALIGNMENTS

RESULT 2 S31866

Systema-1 chain C region - synthetic C;Species: synthetic C;Species: synthetic C;Species: synthetic C,Species: Sylaber C,Species: Sylaber C,Species: Sylaber C,Species: Sylaber C,Species: Sylaber C,Species: Species: Species: Species: Sylaber C,Species: Sylaber C,Spe

Query Match 94.9%; Score 557; DB 4; Length 255; Best Local Similarity 94.5%; Pred. No. 1.5e-47; Matches 104; Conservative 2; Mismatches 4; Indels

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Gaps

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A; Accession: My1723
A; Accession: My1723
A; Rolecule type: protein
A; Rolecule type: protein
A; Rolecule type: protein
A; Rolecule this sequence has the Glm(3) and Glm(non-1) markers
B; Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
Biochemistry 9, 3188-3196, 1970
A; Pitle: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A; Pitle: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A; Pitle: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A; Pitle: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A; Pitle: Schwarz, U.; Ratchel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A; Pitle: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobuline enbromide cleavage products, and the disulfide bridges.
A; Reference number: A91667; WUID: 77070267; PMID: 1002129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin P:20-85/Domain immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C'Species: Homo sapiens (man)
C'Daces 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C'Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J Blochen. 229; 54-66, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;241-310/Domain: immunoglobulin homology <IM3>
F;27-83.144-204,250-2080/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 557; DB 1;
Pred. No. 2.1e-47;
2; Mismatches 4;
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Pred. No. 2.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R_j K hamlichi, A.A. submitted to the EMBL Data Library, September 1994
A; Contents: myeloma protein KOL; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMIM:147100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Contents: annotation; disulfide bonds C, Genetics:
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A,Introns: 99/1; 114/1; 224/1
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Best Local Similarity 94.5%;
Matches 104; Conservative
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A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GDB:120085;
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Best Local Similarity
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A./Accession: B00563.
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A;Residues: 1-330 <ELLb.
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
                                                                                                 39 APELLGGPSVFLFPPKFKDTLMISKTPEVTCVVVDVSHEDPEVKFNWTVDGVEVHNAKTK 98
                                                1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig gamma-1 chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: A93431, S36861; S33887; B90563; A90564; B91668; A91723; A02146 R;Ellison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982 A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A;Reference number: A93433; MuID:82274238; PMID:6287432
                                                                                                                                                                                                                                          R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
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A; Molecule type: protein
A; Molecule type: protein
A; Residues 1.24, E', 26.557, EV', 60-85;132-171, 'ZZZ', 175,'B', 177-193,'D', 195-196,'Q', 198-
A; Note: this sequence has since been revised
R; Hofmann, T.; Parr, D.M.
R; Hofmann, T.; Parr, D.M.
Abol. Immunol. 16, 923-925, 1979
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A; Reference number: A93132; MUID:80114419; PMID:118920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
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A;Gener: GDB:119338; OMIM:147110
A;Gener: GDB:19338; OMIM:147110
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
A;Generiamily: immunoglobulin cregion; immunoglobulin homology
C;Superfamily: immunoglobulin homology cimi>
F;20-85/Domain: immunoglobulin homology cimi>
F;213-202/Domain: immunoglobulin homology cimi>
F;214/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83;140-200,246-304/Disulfide bonds: #status experimental
F;27-83;105,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;27-83;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                          A; Residues: 1-326 <ELL>
A; Residues: 1-326 <ELL>
A; Rossidues: 1-326 <ELL>
A; Cross-references: UNIPROT: P01859; GB: V00554; GB: J00230; NID: G32759; PIDN: CAB58438.1;
A; Note: Lyes-326 is probably removed posttranslationally
A; Oct.; Tung, B.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A; Reference number: A92809; MUID: 81007873; PMID: 6774012
A; Contents: myeloma protein Til
A; Accession: A92809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Title: The amino acid sequences of the three heavy chain constant region domains of A,Reference number: A90752, MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A,Accession: A90752
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Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
A; Fitle: Disulphide bridges of the heavy chain of human immunoglobulin G2. A; Fitle: Disulphide bridges of the heavy chain of human immunoglobulin G2. A; Fontents: annotation; myeloma protein Sa, disulfide bonds
R; Frangione, B.; Milstein, C.; Pink, J.R.L.
A; Frangione, B.; Milstein, C.; Pink, J.R.L.
A; Fitle: Structural studies of immunoglobulin G.
A; Reference number: Asils; MUID:69064124; PMID:5782707
A; Contents: annotation; Sa, disulfide bonds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 < WAN>
A; Note: Trp-156 is at or near the complement-binding site
R; Connell, 'GE.; parr,' D.M.; Hofmann, T.
Can. J. Biochem: 57, 758-767, 1979
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A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
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A;Residues: 238-275 <HOF>
Stylofmann, T; Parry, D.M.
Submitted to the Atlas, March 1980
A;Reference number: A94591
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Best Local Similarity
Matches 102; Conserv
                                                                              A; Molecule type: DNA
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C; Geneticus: 1-30;81-326 cPIN>
C; Geneticus: 1-30;81-326 cPIN>
C; Geneticus: 1-30;81-326 cPIN>
C; Geneticus: 1432.33-14932.33
A; Map position: 14932.33-14932.33
A; Map position: 14932.33-14932.33
A; Introns: 99/1; 111/1; 221/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin c region; immunoglobulin homology <IM1>
F; 20-85/Domain: immunoglobulin homology <IM2>
F; 2134-203/Domain: immunoglobulin homology <IM2>
F; 240-307/Domain: immunoglobulin homology <IM3>
F; 14/Disulfide bonds: interchain (to light chain) #status experimental
F; 27-83, 141-201, 247-305/Disulfide bonds: #status predicted
F; 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Igg gamma-4 chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens Gan) Gallison, J.; Buxbaum, J.; Hood, L. Rillison, J.; Buxbaum, J.; Hood, L. DMA I, 11-18, Jesu Gallison, J.; Buxbaum, J.; Hood, L. DMA I, 11-18, Jesu Gallison, J.; Buxbaum, J.; Hood, L. DMA I, Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene. A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene. A;Reference number: A90933 MID:83157104; PMID:6299662 A;Residues: 1-327 GELL> A;Residues: 1-327 GELL> A;Cross-references: UNIPROT:P01861 A;Note: the sequence was determined from the germline gene R;Pink, J.R. L.; Buttery, S.H.; De Vries, G.M.; Milstein, C. B;Cross-reference managlobulin sublclasses. Partial amino acid sequence of the constant rangelence number: A90249; MUD:70207560; PMID:4192699
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C;Species: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A91906; A92809; Ā90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
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                                                                   111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170
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   Gaps
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                                                                                                                                                                                                                         PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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   Indels
       4
Mismatches
5,
Conservative
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Matches 104; Conservative
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104;
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Matches
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heavy

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A; Modecule type: protein
A; Residues: 1-289 < FRA>
A; Residues: 1-289 < FRA>
A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A; Note: the sequence of residues 42-76 was taken from the reference that follows
B; Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
B; Biol. Chem. 252, 883-889; 1377
A; Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication A; Reference number: A92219; MUID:77118561; PMID:402363
A; Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Note: Cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter R.Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, B.C. Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A.Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the A.Fafrence number: A90198; MUID:77021516; PMID:823945
A.Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Modecule type: protein
A; Residues: 59-125, EB', 128-226, 228-289 < WOL>
A; Residues: 59-125, EB', 128-226, 228-289 < WOL>
A; Residues: 59-125, EB', 128-226, 228-289 < WOL>
A; Rote: Inis protein lacks most of the V region, all of the CHI region, and part of the N; R; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, B.C.; Hood, L.; Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion of A; Reference number: A93915; WUID:82247835; PMID:6808505
A; Contents: heavy chain disease protein Omm
A; Accession: A93915.
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A;Residues: 12-70;72-114;116-125, E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157'
A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A;Residues: 12-97 <MIC>
A;Note: the hinge region in gamma-3 chains is about four times as long as in other
idue segment (12-28)
                 Ig gamma-3 heavy chain disease proteins - human c'Species: Homo sapiens (man)
C'Species: Homo sapiens (man)
C'Species: Homo sapiens (man)
C'Species: J1-Dec-1979 #sequence revision 23-Oct-1981 #text_change 16-Jul-1999
C'Specession: A90442; A92219; A90198; A93915; A02149
E'Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 laceference number: A90442; MUID:81021548; PMID:6774747
A;Contents: heavy chain disease protein Wis
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: jycoprotein; immunoglobulin; pyroglutamic acid
E;203-270/Domain: immunoglobulin homology <IMM>
F;104-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Pred. No. 1e-43;
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Best Local Similarity 86.4%
----hes 95; Conservative
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Ig gamma-3 chain C region (allotype G3m(b)) - human
[Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C; Accession: A23511
R; Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A; Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A; Reference number: A23511; MUID:86148507; PMID:3081877
A; Residues: L-377 <HUC>
A; Residues: 1-377 <HUC>
A; Residues: 1-377 <HUC>
A; Coess-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C; Genetics:
A; Genetics:
A; Genetics: A; Coess-references: GB:M119339; OMIM:147120
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.Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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R; Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A; Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, A; Reference number: A60764; MUID: 90007613; PMID: 2571587
A; Accession: A60764
A; Status: preliminary
A; Mclecule type: DNA
A; Residues: 1-377 cHUC>
A; Cross-references: UNIPROT: 08N4Y9
C; Superfamily: immunoglobulin C region; immunoglobulin homo C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly F; 20-85/Domain: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C; Keywords: immunoglobulin homoly C;
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91.8%; Score 539; DB 2;
Best Local Similarity 90.9%; Pred. No. 1.4e-45;
Matches 100; Conservative 4; Mismatches 6
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F, 20-85/Domain: immunoglobulin homology <IMM>
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gamma

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9
1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                          61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                              Ig gamma 2b chain constant region - pig (fragment)
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81; Conservative
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Matches 79; Conserv
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Best Local S:
Matches 81,
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147160
R;Kacskovics, I:; Sun, J:; Butler, J.E.
J: Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a R;Reference number: 147158; MUID:95015845; PMID:7930579
A;Reference number: 147160
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Rotaus: 1-328 «KAC>
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin c region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147159
19 gamma 2a chain constant region - pig (fragment)
19 gamma 2a chain constant region - pig (fragment)
19 gamma 2a chain constant region - pig (fragment)
2. Species : Sus scrots adomestica (domestic pig)
2. Accession: 147159
3. Seb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C; Accession: 147159
3. Immunol. 153, 3.565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a station region in 147159
A; Reference number: 147159 MUID:95015845; PMID:7930579
A; Accession: 147159
A; Castus: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
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F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Pred. No. 1.2e-37;
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78.8%;
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Best Local Similarity
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A; Residues: 1-328 < KA
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A;Molecule type: mRNA
A;Residues: 1-470 cSAN.
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Rhol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamm
A;Reference number: S06610; MUID:90097956; PMID:2513487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N'Alternate namés: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; Ā31303
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C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                 7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
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A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IPM>
F;181-85/Domain: ammunoglobulin homology <IPM>
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                                                                                                                                                                                                                                                                                                 Length 277;
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                                                                                                                                                                    A,Gene: IgG4
C,Superfamily: immunoglobulin C region; immunoglobulin homology
F,82-151/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, November 1991
A; Reference number: S22080
A; Accession: S22080
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RESULT 15
147158
197158
197158
197158
197158
19 gamma 1 chain constant region - pig (fragment)
C; gamma 1 chain constant region - pig (fragment)
C; gamma 1 chain constant region - pig (fragment)
C; bate: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C; Accession: 147158
R; Kacskovics, I:; Sun, J; Butler, J.E.
J: Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine 1gG identified from the cDNA sequences of a A; Accession: 147158
A; Reference number: 147158; MUID:95015845; PMID:7930579
A; Accession: 147158
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-328 < KAC.
A; Cross-references: EMBL:U03778; NID:9433121; PIDN:AA55216.1; PID:9433122
C; Genetics:
A; Gene: 1gGl
C; Superfamily: immunoglobulin C region; immunoglobulin homology
F; 133-202/Domain: immunoglobulin homology < IMM>
C;Accession: 147161
R;Kacskovics, I; Sun, J; Butler, J.E.
J Immunol. 153, 3565-3573, 1994
A;Time: 153, 3565-3573, 1994
A;Time: 153, 3565-3573, 1994
A;Time: 154, 1954
A;Time: 157, 1956-3573, 1994
A;Reference number: 147158; MUD:95015845; PMID:7930579
A;Reference number: 147161
A;Reference number: 147161
A;Residues: 147161
A;Residues: 1-328 (ARA-A;Residues: 1-328 (AR
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Q6n030 Q8nf17 Q8nf17 Q8n4y9 Q6n4y9 Q6n4y9 Q95m34 Q95m34 Q95m34 Q95m32 Q6kam2 Q6kam2 Q7186 Q91987 Q7186 Q9186
Q8N4Y9 Q68CN4 GC3 HUMAN Q95M34 GCB RAT GC RABIT GCZ CAVPO

Q6KAM2 GC3_MOUSE MOUSE

GC3M

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GCB MOUSE

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Name=IGHG1;
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P01857;
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      GenCore (c) 1993
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SEQUENCE (MYELOMA PROTEIN NIE).
MEDLINE=770070269; PubMed=826475;
Ponsting1 H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                                                                                                                                                                                                                                                                                                                                               VII. Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The covalient structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; Biochemistry 9:3171-3181 (1970).
                                                                                                                                                                                                                                                                      immunoglobulin C gammal gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schwidt W.E., Jung H.-D., Pallm W., Hilschmann N.; "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."; Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                           Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                     "The covalent structure of a human gamma G-immunoglobulin. VII acid sequence of heavy-chain cyanogen bromide fragments H1-H4. Biochemistry 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=71064025; PubMed=5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigaberg W.H.,
Edelman G.M.;
                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
Cunningham B.A., Rutiahauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS. MEDLINE=83289131; PubMed=6884994;
                                                     (Rel. 01, Last sequence update) (Rel. 45, Last annotation update)
 330 AA
                                                                                                                                                                                                                                 MEDLINE-82274238; Pubmed=6287432;
Blison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human imm
Nucleic Acids Res. 10:4071-4079(1982).
 PRT;
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DISULFIDE BONDS.
MEDLINE=71064027; PubMed=4923144;
                                     (Rel. 01, Created)
                                                                                                                                    nomo bapiens (numan).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                      25-OCT-2004 (Rel. 45, Lasig gamma-1 chain C region
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 136-329 (EU)
                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                 21-JUL-1986 (
21-JUL-1986 (
25-OCT-2004 (
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homo sapien homo sapien

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Q6mzx7 P01859

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06p6c4 06mzu6 086tt2

Q6P6C4 Q6MZU6 Q86TT2

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06PJF1 06N097 072351 06PJ95 096PQ8 096PQ8 08N096 GC4 HUMAN 08TC63 065ZL2 065ZL2 066ZZL2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residues
residues
                                                                                                                                                                                                                                                                                                                                                      Descender J.;

"Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";

Biochemistry 20:2361-2370(1981).

-! MSCELLANBOUS: Nie has the GIM(17) allotypic marker, 97-K, and the GIM(3) markers, 239-D and 241-L. KOL and EU sequences have the GIM(3) marker and the GIM (non-1) markers.

-! MISCELLANBOUS: Nie also differs in the amidation states of 35, 116, 198, 269 and 272.

-! MISCELLANBOUS: EU also differs in the amidation states of residues 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
                                                                                                           DISULFIDE BONDS.

MEDILINE=77070267; PubMed=1002129;

MEDILINE=77070267; PubMed=1002129;

Dreker L., Schwarz J., Reichel W., Hilschmann N.;

Rule of antibody structure. The primary structure of a monoclonal 19G1 immunoglobulin (myeloma protein Nie), I: purification and reharacterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: KOL also differs in the amidation states of
                      "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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MEDLINE=81208100; PubMed=7236608;
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PDB; IDA71; X-ray; H=1-103.
PDB; IDS1; X-ray; H=1-101.
PDB; IDS1; X-ray; H=1-101.
PDB; IDS1; X-ray; H=1-101.
PDB; IDNX; X-ray; A/B=10-329.
PDB; IPC2; X-ray; A/B=106-329.
PDB; IFC2; X-ray; A/B=106-329.
PDB; IFC2; X-ray; A/B=106-329.
PDB; IFC2; X-ray; B/D=1-103.
PDB; IITS; X-ray; B/D=1-103.
PDB; IITS; X-ray; B/D=1-103.
PDB; IITS; X-ray; A/B=10-330.
PDB; IIX; X-ray; A/B=10-330.
PDB; IOXX; X-ray; A/B=10-330.
PDB; IOXX; X-ray; A/B=10-330.
PDB; IOXX; X-ray; A/B=10-326.
PDB; IOXX; X-ray; A/B=10-330.
PDB; ICX; X-ray; A/B=10-330.
PDB; ICX; X-ray; A/B=10-330.
PDB; ICX; X-ray; A/B=10-330.
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      ., Edelman G.M.;
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K -> R (in GlM(3) marker).
FTIGAVAR 00388.
D -> E (in GlM(non-1) marker).
FTIGAVAR 003887.
L -> M (in GlM(non-1) marker).
FTIGAPAR_003888.
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            (with light chain)
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Pred. No. 3.5e-47;
2; Mismatches 4; Indels
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NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS70731; AAS88328.1; -.
HSSP; P01857; 1AJ7.
                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hepatitis B virus receptor binding protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 AA; 38162 MW; DD96C3D7E0BE5845 CRC64;
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94.5%; Pred. No. 3.8e-47;
iive 2; Mismatches 4;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig-c1.
InterPro; IPR003006; Ig-mHC.
Pfam; PF07654; C1-8et; 3
SWART; SW00407; IGC1; 3
PROSITE; PS06835; IG_LIKE; 3
PROSITE; PS06290; IG_MHC; UNGNOWN_2.
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                                                                                                                                                         PRELIMINARY;
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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05-JUL-2004
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NON TER
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Q6PYX1
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249 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 308
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Ghaley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Shakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Rzywinski M.I., Skabaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., McKernen K.J., Malek J.A., Gunaratne P.H.,
Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strauberg R., Strauberg R., Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL, BC073766; AAH73766.1; ... InterPro; IPR003599; Ig. InterPro; IPR003597; Ig.cl. InterPro; IPR003597; Ig.cl. InterPro; IPR003506; Ig.MHC. InterPro; IPR003596; Ig. WHC. InterPro; IPR003596; Ig. WHC. InterPro; IPR003596; Ig. WHC.
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Last sequence update)
Last annotation update)
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Pfan, PP00047; ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00406; IG21; 3.
SMART; SM00406; IGV; 1.
PROSITE; PSSO835; IG_LIKE; 4.
PROSITE; PSSO8290; IG_MHC; UNKNOMN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                      cDNA sequences.
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Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Primary B-Cells;
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Q6PJA4
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A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Ridendul S.F., Zeeberg B., Grouse L.H., Schaefer C.F., Bhat N.K.,
A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Stapleton M., Soares M.B., Pandldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ubdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | InterPro; IRR00110; Ig-like. | InterPro; IRR00110; Ig-like. | InterPro; IRR00110; Ig-like. | InterPro; IRR00110; Ig-like. | InterPro; IRR0013006; Ig-MrC. | InterPro; IRR001306; Ig-WrC. | InterPro; IRR001609; Ig-WrC. | InterPro; IRR00409; IG-2. | SWART; SW00400; IG-2. | SWART; SW00400; IG-2. | SWART; SW00406; IG-2. | SWART; SW00406; IG-2. | SWART; SW00406; IG-2. | SWART; SW00406; IG-2. | SWART; SW00406; IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. | IG-2. 
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Peripheral Nervous System;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072419; AAH72419.1; -.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                               and mouse cDNA sequences."
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Best Local S
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A STEAMURE FROM N.A.

TISSUE=Primary B-Cells;

AN EDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altscherko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatcherko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., McDan P.J., McKernen K.J., Malek J.A., Gunaratne P.H.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Nillalon D.K., Muzny D.M., Scheryen B.J., Lu X., Gibbs R.A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Norley S.J., Marra M.A.;

A Jones S.J., Marra M.A.;

A Green S.J., Marra M.A.;

A Mones S.J., Marra M.A.;

A Mones S.J., Marra M.A.;

A Mones C.M. Schmertion B.E., Schnerch A., Schein J.E.,

A Mar M.A.
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
REMBL, BC051328; AAH51328.1; -.
REMBL, BC051328; AAH51328.1; -.
RINEEPPO; IPR007110; Ig-like.
RINEEPPO; IPR003597; Ig-C1.
RINEEPPO; IPR003596; Ig-MHC.
RINEEPPO; IPR003596; Ig-WHC.
REMPT, SM00406; Ig-V.
REMRT; SM00406; IGV; 1.
RPC051TE; PS550835; IG-LIKE; 4.
RPC051TE; PS002905; IG-LIKE; 4.
RPC051TE; PS002905; IG-LIKE; 4.
SEQUENCE 469 AA; 51395 MW; C8D58E12BAAF795C CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Best Local Similarity 94.5<sup>3</sup>
Matches 104; Conservative
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Homo sapiens (Human).
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                                                                                                                                                                                                   Proc. Natl. Acad.
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Q6N089
Q6N089;
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Matches
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A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Boarles R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Brownstein M.J., Usdin T.B., Toobhiyuki S., Carninci P., Prange C.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Phitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krayninski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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"Generation_and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                             Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC018747; AAH18747.1; -. HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE. 470 AA; 51715 MW; 7B49556AllFD7D99 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.9%; Score 557; DB 2; .94.5%; Pred. No. 5.3e-47; tive 2; Mismatches 4;
                                                                                                                                    InterPro; IPR003159; IG.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003596; Ig_WC.
InterPro; IPR003596; Ig_WC.
InterPro; IPR003596; Ig_V.
InterPro; IPR003596; Ig_V.
INTERPRO$ IG 2 3 SWART; SW00406; IG; 2 1 SWART; SW00406; IG; 2 1 PR05ITE; PS003596; IG_LIKE; 4.
IPRO$ITE; PS00390; IG_MHC; UNKNOWN_2.
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Best Local Similarity 94.51
Matches 104; Conservative
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SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
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Homo sapiens (Human).
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Strausberg R.;
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01-OCT-2003 (
01-OCT-2003 (
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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The German Human cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Exempted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

REMBL, BC053984; AAH53984.1; -. RHSSP, PO1877; 1HZH.

R InterPro; IPR00110; Ig-like.

R InterPro; IPR003597; Ig_c1.

R InterPro; IPR003596; Ig_W.

R InterPro; IPR003566; Ig_W.

R Pfam; PF07654; C1-set; 3.

R RAMAT; SM00406; IGV; 1.

R PROSITE; PS0239; IG_MHC; UNKNOWN_2.

R PROSITE; PS0239; IG_MHC; UNKNOWN_2.

HYPOTCHELICAL PROSIDE:

W HYPOTCHELICAL PROSIDE:

SEQUENCE 470 AA; 51204 MW; 778CP34521483E1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 94.9%; Score 557; DB 2; Length 470; Best Local Similarity 94.5%; Pred. No. 5.3e-47; Matches 104; Conservative 2; Mismatches 4; Indels
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Lubmitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; BX64627; CAE45781.1; -.

R HSSP, P01661; 1AD0.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003596; Ig.

R InterPro; IPR003596; Ig.

R SMART; SM00409; Ig.

R SMART; SM00409; IG.

R SMART; SM00409; IG.

R SMART; SM00409; IG.

R SMART; SM00409; IG.

R SMART; SM00409; IG.

R SMART; SM00406; IG.

R SMART; SM00406; IG.

R SMART; SM00406; IG.

R SMART; SM00406; IG.

R SMART; SM00406; IG.

R SMART; SM00406; IG.

R SMOSITE; PS50835; IG.

R PROSITE; PS508290; IG.

R Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheical protein DKFZp686P15220.
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94.5%; Pred. No. 5.3e-47;
iive 2; Mismatches 4;
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les 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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and mouse cDNA
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Q6GMW7
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                                                                                                                                                                                                           to SEQUENCE FROM N.A.

TISSUE=Human small intestine;

TISSUE=Human cDNA Consortium;

The German Human cDNA Consortium;

A Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

B Boecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

L Submitted (Aug-2003) to the EMBL/GenBank/DDBJ databases.

S EMBL; BX640852; CA645920.1; -.

R EMBL; BX640852; CA645920.1; -.

R INCEPTO: IPR00310; Ig.

R INCEPTO: IPR00310; Ig.

R INCEPTO: IPR003597; Ig.

R INCEPTO: IPR003596; Ig.

R INCEPTO: IPR003596; Ig.

R INCEPTO: IPR003596; Ig.

R INCEPTO: IPR003596; Ig.

R INCEPTO: IPR003596; Ig.

R SWART; SW004007; IG.: 3.

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TISSUB-Peripheral Nervous System;
MEDLINE-22388257, PubMed-12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257, PubMed-12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 AA; 52121 MW; 9476EAE4COBFC447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                     Last sequence update)
Last annotation update)
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94.9%; Score 557; DB 2;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4.
                                                                473
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                           Created)
                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
Hypothetical protein DKFZp686C11235.
Name-DKFZp686C11235;
                                                               PRT;
                                                                                       05-JUL-2004 (TrEMBLrel. 27,
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                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
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                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
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Q6P055;
                                                                                Q6MZV7;
                                                                Q6MZV7
                                          RESULT 9
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257 APELLGGPSVFLFPPKRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 316
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Baha S.S., Loquellano N.A., Peters G.J., Abramon R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Madan A., Woung A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
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TISSUE-Spleen,

TISSUE-Spleen,

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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Hypotherical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases EMBL, BC065820, AAH65820.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 AA; 51344 MW; 9816D56A77129B57 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.9%; Score 557; DB 2;
94.5%; Pred. No. 5.3e-47;
iive 2; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001359; IG.
InterPro; IPR001359; IG.
InterPro; IPR00110; IG-like.
InterPro; IPR001359; IG_d.
InterPro; IPR003596; IG_d.
InterPro; IPR003596; IG_d.
InterPro; IPR003596; IG_w.
Pfam; PF07654; Cl-set; 3.
SWART; SW00400; IG; 2.
SWART; SW00400; IG; 2.
SWART; SW00400; IGv; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 473 AA; 51344 MW; 9816D56A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Peripheral Nervous System;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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hes 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC065820; AAH
HSSP; P01861; 1ADQ.
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Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
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Q6GMX1
                S X R R R R R S
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Human esophagus tumor;
The German Human cDNA Consortium;
Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                              Straubbergrey,
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
REAL, BCO73782; AAH73782.1;
InterPro; IPR001599; Ig-1ike.
RINTERPRO; IPR001100; Ig-1ike.
RINTERPRO; IPR003597; Ig_c1.
RINTERPRO; IPR003596; Ig_wHC.
RINTERPRO; IPR003596; Ig_v.
R Pfam; PF00467; ig; 4.
R SWART; SW00409; IG; 2.
R SWART; SW00409; IG; 1.
R RART; SW00409; IG; 1.
R RROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 94.9%; Score 557; DB 2; Length 475; Best Local Similarity 94.5%; Pred. No. 5.3e-47; Matches 104; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (1907-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640947; CAE45972.1; -...
HSSP; PO1861; 1ADQ.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig-11ke.
InterPro; IPR003597; Ig-61.
InterPro; IPR003597; Ig-61.
InterPro; IPR003596; Ig-MC.
InterPro; IPR003596; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al protein.
475 Aa; 51987 MW; 2AlFE55D736860F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686G11190.
                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                  TISSUE-Spleen;
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SEQUENCE 47
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Fobo G., Han M., Wiemann S.;
Fobo G., Han M., Wiemann S.;
Fobo G., Han M., Wiemann S.;
Fobo G., Han M., Wiemann S.;
Fobo G., Han M., Wiemann S.;
Fobo G., Han M., Wiemann S.;
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Fob G., Han M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., Miemann M., 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                            94.9%; Score 557; DB 2; Length 47 94.5%; Pred. No. 5.3e-47; rative 2; Mismatches 4; Indels
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Pfam; PF07654; Cl-set; 3.

SMART; SM00409; IG; 2.

SMART; SM00400; IGcl; 3.

SWART; SM00406; IGv, 1.

PROSTTE; PS50835; IG LIKE; 4.

PROSTTE; PS00290; IG_MHC; UNKNOWN_2.

Hypothetical protein:

SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;
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SEQUENCE 475 AA; 52360 MW; 7BA14104CD2DB8F0 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheital protein DKF2p686K03196.
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94.5%; Pred. No. 5.3e-47;
iive 2; Mismatches 4;
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The German Human cDNA Consortium;
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Matches 104; Conservative
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Matches 104; Conservative
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05-JUL-2004 (TrEMBLrel.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MALEAUBERT R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Nilalon D.K., Muzny D.M., Schwuchenko Y., Boutfard G.G.,
Radriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,
Annes S.J., Marra M.A.;
Jones S.J., Marra M.A.;
and mouse CDNA sequences.
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                                                                                                                                                                                                                                                        Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
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                                                                                     Created)
Last sequence update)
Last annotation update)
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94.9%; Score 557; DB 2;
Best Local Similarity 94.5%; Pred. No. 5.3e-47;
Matches 104; Conservative 2; Mismatches 4
                 476 AA
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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InterPro; IRR003599; Ig.
InterPro; IRR003599; Ig.
InterPro; IRR003106; Ig_MHC.
InterPro; IRR003586; Ig_V.
Pfam; PF07654; C1-set; 3.
Pfam; PF07654; C1-set; 3.
SMART; SM00407; IG; 4.
SMART; SM00407; IG; 3.
                                                                                     05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                 PRELIMINARY;
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                                                                                                                                                                                        Hypothetical protein. Homo sapiens (Human).
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TISSUE=Primary B-Cells;

MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Alschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Alschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Antichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Dordan H., Moore T. Max S.I., Wang J., Hisieh F., Dordan H., Moore T. Max S.I., Wang J., Hisieh F., Dordan H., Moore T., Scheetz T.E., Anderson M.J., McKernan K.J., Malak J., Prange C., Anderson R.J., Marang D.M., Sodergren E.J., Marang R.M., Hullahy S.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A. C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Arzwinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

Menseration and initial analysis of more than 15,000 full-length human
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94.5%; Pred. No. 5.4e-47;
ive 2; Mismatches 4; Indels
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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SEGUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;
27, Last sequence update)
27, Last annotation update)
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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InterPro; IPR003599; Ig.
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Best Local Similarity 94.5
Matches 104; Conservative
                                                              05-JUL-2004 (TrEMBLrel.
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                                                                                                                  Hypothetical protein.
Homo sapiens (Human).
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Search completed: November 17, 2005, 07:10:20 Job time: 81.6164 secs

478 AA.

Q6P181; 05-JUL-2004 (TrEMBLrel. 27, Created)

PRELIMINARY;

Q6PI81 RESULT 15 Q6PI81 ID Q6PI8: AC Q6PI8 DT 05-JU

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US-09-841-221A-2
US-09-1704A-2
US-09-170-1704A-2
US-09-122-144-2
US-09-122-144-2
US-09-122-144-2
US-09-121-247-6
US-09-131-247-6
US-09-131-247-6
US-09-131-247-6
US-09-131-247-6
US-09-131-247-6
US-09-131-247-6
US-09-138-082B-1068
US-09-428-082B-1058
US-09-428-082B-1058
US-09-428-082B-1058
US-09-428-082B-1068
US-09-428-082B-1068
US-09-428-082B-1068
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Sequence 22, Application US/09968362A
Batent No. 6/97493
Batent No. 6/97493
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL Sun, Bill
APPLICANT: Sun, Bill
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor
TITLE OF INVENTION: increased biological activities
FILE REFERENCE: 03SUN2001
CURRENT APPLICATION NUMBER: US/09/968,362A
CURRENT FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: hG-CSF-L-vFc gammal with a 30-amino acid leader peptide (Figure 2 ; OTHER INFORMATION: C)
US-09-968-362A-22
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Sequence 67, Application US/09485737B

Sequence 67, Application US/09485737B

Sequence 67, Application US/09485737B

SEQUENCE NOT SASONO.

TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK, TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK, TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

FILLE REFERENCE: INNS:015

CURRENT APPLICATION NUMBER: US/09/485,737B

CURRENT PILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: PCT/EP 98/05165
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Pred. No. 3.9e-59;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.1%;
97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 97.33
Matches 107; Conservative
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US-09-499-846-12
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Sequence 67, Application US/10071485

Sequence 67, Application US/10071485

Sequence 67, Application US/10071485

GENERAL INFORMATION:

APPLICANT: BUYER, Marie-Ange

APPLICANT: BUYER, Marie-Ange

TITLE OF INVENTION: SHOCK,

TITLE OF INVENTION: SHOCK,

TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

FILE REFERENCE: INNS:015

CURRENT APPLICATION NUMBER: US/10/071,485

CURRENT PILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: PCT/FP 98/05165

PRIOR PILING DATE: 1998-08-14

PRIOR PILING DATE: 1998-06-14

PRIOR PILING DATE: 1999-06-18

PRIOR RILING DATE: 1999-06-18

PRIOR PILING DATE: 1999-06-18

PRIOR PILING DATE: 1997-08-18

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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.7%; Score 562; DB 3; Length 46 Best Local Similarity 95.5%; Pred. No. 3.7e-58; Matches 105; Conservative 2; Mismatches 3; Indels
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Pred. No. 3.7e-58;
2; Mismatches 3.
  PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION WUMBER: EPO 98870139.7
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PATCHTIN VERSION 3.0
SEQ ID NO 67
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Best Local Similarity 95.5%;
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: SYNTHETIC US-09-485-7378-67
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US-10-071-485-67
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RESULT

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Best Local Similarity 95.3%; Pred. No. 3.9e-58;
Matches 105; Conservative 2; Mismatches 3; Indels
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95.5%; Pred. No. 4e-58;
tive 2; Mismatches 3; Indels
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Sequence 10, Application US/09499846

Sequence 10. Application US/09499846

Sequence 10. 6656728

GENERAL INFORMATION:

APPLICANT: Kavanaugh et al.

TITLE OF INVENTION: RECEPTOR-IMMUNGLOBULIN FUSION

TITLE OF INVENTION: RECEPTOR-IMMUNGLOBULIN FUSION

TITLE OF INVENTION: NEGEPTOR-IMMUNGLOBULIN FUSION

TITLE OF INVENTION: RECEPTOR-IMMUNGLOBULIN FUSION

TITLE OF INVENTION: RECEPTOR-IMMUNGLOBULIN FUSION

TITLE OF INVENTION: NUMBER: US/09/499, 846

CURRENT APPLICATION NUMBER: US/09/499, 846

CURRENT FILING DATE: 2000-02-07

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 10

LENGTHARE: FastSEQ for Windows Version 3.0

LENGTH: 497
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US-09-446-8
US-09-449-846-8
; Sequence 8, Application US/09499846
; Patent No. 6656728
; GENERAL INPORMATION:
; TITLE OF INVENTION: PIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; TILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
                                                                                 APPLICANT: Kavanaugh et al.
TITLE OF INVENTION: FIEROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR:IMMUNGGLOBULIN FUSION
FILE REPERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
Sequence 12, Application US/09499846
Patent No. 6656728
GENERAL INFORMATION:
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Best Local Similarity 95.55
Matches 105; Conservative
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US-09-499-846-10
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-09-968-362A-20
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US-09-485-7378-90

i Sequence 90, Application US/09485737B

i Sequence 90, Application US/09485737B

i Sequence 90, Application US/09485737B

i GENERAL INFORMATION:
    TELE OF INVENTION: Expin

    TITLE OF INVENTION: ACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

    TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

    CURRENT APPLICATION NUMBER: US/09/485,737B

    CURRENT PILING DATE: 1998-06-14

    PRIOR PILING DATE: 1998-06-14

    PRIOR FILING DATE: 1998-06-18

    PRIOR FILING DATE: 1998-06-18

    PRIOR FILING DATE: 1998-06-18

    PRIOR FILING DATE: 1999-06-18

    PRIOR FILING DATE: 1997-08-18

    NUMBER OF SEQ ID NOS: 104

    SOFTWARE: PATCHIN UNIVER: DEPO 370122.5

    NUMBER OF SEQ ID NOS: 104

    SEQ IDN OS: 104

    SEQ IDN OS: 104
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Sequence 90, Application US/10071485
Fatent No. 6813052
GENERAL INFORMATION:
APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC:
TITLE OF INVENTION: SABCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                        1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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                                                                                                                                                                                      Score 562; DB 4; Length 52
Pred. No. 4.3e-58;
2; Mismatches 3; Indels
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95.5%; Pred. No. 6.5e-58;
tive 2; Mismatches 3.
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 525
                                                                                                                                                                                    Query Match 95.7%;
Best Local Similarity 95.5%;
Matches 105; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90
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Matches 105; Conservative
                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 20, Application US/09968362A

Fatent No. 6797493

GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Bill
APPLICANT: Sun, Cecliy R

TITLE OF INVENTION: increased biological activities
TITLE OF INVENTION: increased biological activities
FILE REFERENCE: 03SUNZO1

CURRENT APPLICATION NUMBER: US/09/968,362A

CURRENT APPLICATION NUMBER: US/09/968,362A

CURRENT APPLICATION NUMBER: 2001-10-01

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.1

SEQ ID NO 20

LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure 2 OTHER INFORMATION: B)
US-09-966-3621-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.5%; Pred. No. 6.5e-58;
Matches 105; Conservative 2; Mismatches 3
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/10/071,485
CURRENT FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 09/485,737
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 1900-08-14
PRIOR PILING DATE: 1998-08-14
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SQTTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: SYNTHETIC US-10-071-485-90
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RESULT 10 US-09-746-359A-62

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Query Match
94.9%; Score 557; DB 3; Length 110;
Best Local Similarity 94.5%; Pred. No. 2.1e-58;
Matches 104; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                      Score 558; DB 4; L. Pred. No. 1.5e-57; 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING JATE
FILING JATE
FILING JATE
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAWE: WAGNEY, RICHARY
REGISTRATION NUMBER: 34,40
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION: NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               US-08-444-644-21
; Sequence 21, Application US/08444644
; Patent No. 6015555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617) 861-6240
                                           Query Match
Best Local Similarity 95.5%;
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02173
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US-09-746-359A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.1%; Score 558; DB 4; Length 559; 95.5%; Pred. No. 1.4e-57; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                         APPLICANT: Began, Maribeth A.
APPLICANT: Began, Maribeth A.
APPLICANT: Candrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: No. 6610286ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation FILE REPERENCE: 99-108
CURRENT FILING DATE: 201-05-21
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-33
PRIOR FILING DATE: 1999-12-33
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Melly, James D.
APPLICANT: Blumberg, Hal
APPLICANT: Blumberg, Hal
APPLICANT: Bagner, Maribeth A.
APPLICANT: Bagner, Stephen R.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: No. 6610286ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation FILE REFERENCE: 99-108
CURRENT APPLICANTION NUMBER: US/09/746,359A
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/171,969
FRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARR: FASTESEQ for Windows Version 3.0
LENGTH: 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/09746359A Patent No. 6610286
     Application US/09746359A
                                                                            APPLICANT: Thompson, Penny
APPLICANT: Poster, Donald C.
APPLICANT: Werfeng
APPLICANT: Madden, Karen L.
APPLICANT: Kally, James D.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Blumberg, Hal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xu, Wenfeng
Madden, Karen L.
Kelly, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thompson, Penny APPLICANT: Foster, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.5
Matches 105; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-09-746-359A-23
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          Sequence 62,
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APPLICANT:
APPLICANT:
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APPLICANT:
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ITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

TITLE OF INVENTION: CONJUGATES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                Length 594;
                                         Indels
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US-08-232-539D-55
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1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                      1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

TITLE OF INVENTION: CONJUGATES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                    61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWAREI Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,246A

FILING DATE: 04-MAY-1994

CLASSIPICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/800,458

FILING DATE: 26-MOV-1991

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: PCT/US90/05077

FILING DATE: 07-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

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APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/404,089

FILING DATE: 07-SEP-1989

ATOMNEY MAGNATION:

NAME: NAME: WARDANEY NUMBER: US 07/404,089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 94.9%; Score 557; DB 3; Best Local Similarity 94.5%; Pred. No. 2.1e-58; Matches 104; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
TELEFANCE (617) 861-9540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARCTERISTICS:
LENGTH: 110 amino acids
                                                                                                                                                                                                                                                                                              Sequence 21, Application US/08232246A Patent No. 6329508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                          RESULT 13
US-08-232-246A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-232-246A-21
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                                                         STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COUNTRY: USA

ZIP: 98101

CONPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1

SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION NUMBER: US/08/430,633

FILING DATE: 28-APR-1995
CLASSIFICATION: 43-5

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/235,397
FILING DATE: 04/28/94

ATTORNEY/AGENT INFORMATION:
MAME: PETKINS, PATAICIA A.
REFERENCE/DOCKET NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2612

TELECPHONE: (206) 587-0430

TELECPHONE: (206) 533-0644

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: CLONE: 1961 FC

ORGANISM: Human
INMEDIATE SOURCE:
ORGANISM: Human
INMEDIATE SOURCE:
CLONE: 1961 FC

US-08-430-633-4
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.5
Matches 104; Conservative
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Search completed: November 17, 2005, 07:13:22 Job time : 25.6119 secs

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LENGTH: 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                   1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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- 2005 Compugen Ltd
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US-10-959-318-10

US-11-102-403-25

US-09-932-812-22

US-10-761-593A-22

US-11-016-518A-22

US-11-017-185-22

US-09-968-362-22

US-10-800-497-22

US-10-800-497-22

US-10-800-497-22

US-10-800-497-22
                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                     1867879 seqs, 418409474 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       protein search, using sw model
                                                                                                                                                 Gapop 10.0 , Gapext 0.5
  GenCore
Copyright (c) 1993
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seq length: 200000000
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US-10-959-318-11
US-10-959-318-12
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US-10-683-255-12
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US-10-988-380-38
US-10-1018-102-25
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ALIGNMENTS

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Publication No. US20030082749A1
Publication No. US20030082749A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: For fusion proteins of human erythropoietin with increased biologi
FILE REFERENCE: 02SUN001
CURRENT APPLICATION NUMBER: US/09/932,812
CURRENT APPLICATION NUMBER: 2011-10-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
FURTHER PATENTIAL SUN APPLICATION OF SEQ ID NOS: 22
SEQ ID NOS: 22
SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: HuEPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2C US-09-932-812-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/10761593A

Sequence 22, Application US/10761593A

Sequence 22, Application US/20040175824A1

GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Cecily R

TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
TITLE OF INVENTION: activities
FILE REFERENCE: 025UN2001-A

CURRENT APPLICATION NUMBER: US/10/761,593A

CURRENT PILING DATE: 2004-01-21

PRIOR PILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.2

SEQ ID NO 22

LENGTH: 435
                                                                                                                                                                                                      114 APPVA-GPSVFLFPPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 APBVAGGPSVFLFPPKPKDTLMISKTPEVTCVVVDVSHEDPBVKFNWYVDGVEVHNAKTK 278
                                                                                                                                                                    1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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                                                                  DB 20; Length 329;
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                                                                  Score 570.5; DB 20;
Pred. No. 2.5e-47;
0; Mismatches 0;
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97.3%; Pred. No. 3.8e-47;
tive 1; Mismatches 2;
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                  Query Match
Best Local Similarity 99.1%;
Matches 109; Conservative
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Best Local Similarity 97.3
Matches 107; Conservative
; ORGANISM: Homo sapiens
US-11-102-403-25
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OTHER INFORMATION: mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APPVAGGPSVFLFPPKPKDYLMISRTPEVTCVVVDVSEEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                              RESULT 2
US-10-959-318-10
| Sequence lo, Application US/10959318
| Publication No. US2050215/68A1
| GENERAL INFORMATION:
| APPLICANT: Armour, Kathryn L
| APPLICANT: Clark, Michael R
| TITLE OF INVENTYON: POlypeptides including modified constant regions
| FILE REFERENCE: 39-302
| CURRENT APPLICATION NUMBER: US/10/959,318
| CURRENT FILING DATE: 2004-10-07
| PRIOR FILING DATE: 2004-10-07
| PRIOR FILING DATE: 2003-10-17
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 10
| LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APPVAGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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                            PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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APPLICANT: STERN, ANNE
APPLICANT: STREIN, PAMELA
APPLICANT: STUBENRAUCH, KAY-GUNNAR
APPLICANT: VAN DE WINKEL, JAN
APPLICANT: VAN VUGT, MARTINE
TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/11/102,403
CURRENT FILING DATE: 2005-04-08
PRIOR PILING DATE: 2004-04-13
PUNBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 25
LENGTH: 329
TYPE: PRI
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JANSEN-MOLENAAR, MIRANDA
KLING, DOROTHEE
KOPETZKI, ERHARD
PARREN, PAUL
REBERS, FRANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 25, Application US/11102403; Publication No. US20050226876A1; GENERAL INFORMATION:
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Matches 109; Conservative
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US-11-102-403-25
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FEATURE:
OTHER INFORMATION: HuEPO-L-VFc gammal with a 27-amino acid leader peptide (Figure 20)
OTHER INFORMATION: )
US-11-017-185-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: hG-CSF-L-vFc gammal with a 30-amino acid leader peptide (Figure 2; OTHER INFORMATION: C)
US-09-968-362-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill
APPLICANT: Sun, Bill
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor
TITLE OF INVENTION: biological activities
FILE REFERENCE: 03SUN2001
CURRENT APPLICATION NUMBER: US/09/968,362
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                               219 APEVAGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 278
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APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-
TITLE OF INVENTION: increased biological activities
FILE REPERENCE: 035UN2001
CURRENT APPLICATION NUMBER: US/10/800,497
CURRENT FILING DATE: 2004-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                    PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Pred. No. 3.9e-47;
1; Mismatches 2;
                                                                                                                                                                                                            Score 570; DB 20;
Pred. No. 3.8e-47;
                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 22, Application US/09968362; Publication No. US20030082679A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/10800497; Publication No. US20040259209A1; GENERAL INFORMATION:
                         LENGTH: 435
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 97.3%;
Matches 107; Conservative
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97.1%;
Best Local Similarity 97.3%;
Matches 107; Conservative
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         SEQ ID NO 22
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Publication No. US20050142642A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Activities
TITLE OF INVENTION: activities
TITLE OF INVENTION: activities
CURRENT APPLICATION NUMBER: US/11/017,185
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US/01-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
  HuBPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: HuEPO-L-vFc gammal with a 27-amino acid leader peptide (Figure ; OTHER INFORMATION: 2C)
US-11-016-518A-22
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/11016518A

Publication No. US20050124045A1

GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Cecily R

TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased
TITLE OF INVENTION: Polological activities
FILE REFERENCE: 025UN2004D1

CURRENT APPLICATION NUMBER: US/11/016,518A

CURRENT PAPLICATION NUMBER: US/09/932,812

PRIOR APPLICATION NUMBER: US/09/932,812

PRIOR FILING DATE: 2001-08-17

PRIOR FILING DATE: 2001-08-17

SOFTWARE: Patentin version 3.2

SEQ ID NOS: 28

SEQ ID NOS: 28

SEQ ID NOS: 28
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                                                                                                                                                                                1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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                                                                                         Score 570; DB 16;
Pred. No. 3.8e-47;
1; Mismatches 2;
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Pred. No. 3.8e-47;
1; Mismatches 2;
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                                                                                       Query Match
Best Local Similarity 97.3%;
Matches 107; Conservative
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Matches 107; Conservative
; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-761-593A-22
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US-11-016-518A-22
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US-11-017-185-22
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OTHER INFORMATION: Variant of Human 1gG1 CH2 sequence with delta c and e (E268) OTHER INFORMATION: mutations
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Sequence 14, Application US/10959318

Publication No. US20050215768A1

GENERAL INFORMATION:

APPLICANT: Armour, Kathryn L

APPLICANT: Clark, Michael R

TITLE OF INVENTION: Polypeptides including modified constant regions

FILE REPERENCE: 39-302

CURRENT APPLICATION NUMBER: US/10/959,318

CURRENT PILING DATE: 2004-10-07

PRIOR PLICATION NUMBER: PCT/GB2004/004254

PRIOR PLIUNG DATE: 2004-10-07

PRIOR PLIUNG DATE: 2004-10-07

PRIOR PLIUNG DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.3

SOFTWARE: PATENTING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTING DATE: 2003-10-17

SOFTWARE: PATENTING DATE: 2004-10-07

SOFTWARE: PATEN
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IITLE OF INVENTION: Polypeptides including modified constant regions
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96.3%; Score 565; DB 18; Length 110;
Best Local Similarity 96.4%; Pred. No. 2.4e-47;
Matches 106; Conservative 1; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 110;
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Pred. No. 2.4e-47;
1; Mismatches 3;
                                       FILE REFERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT PILLIG DATE: 2004-10-07
PRIOR APPLICATION NUMBER: PCT/GB2004/004254
PRIOR PILLING DATE: 2004-10-07
PRIOR PILLING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: GB0324368.0
PRIOR SELING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Variant of OTHER INFORMATION: mutations
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Best Local Similarity 96.4%;
Matches 106; Conservative
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LENGTH: 110
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US-10-959-318-7
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; Sequence 22. Application Wo. UG20040265973A1
; Sequence 22. Application No. UG20040265973A1
; Bublication No. UG20040265973A1
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: For fusion proteins of human granulocyte colony-stimulaing factor; TITLE OF INVENTION: increased biological activities
; TITLE OF INVENTION: increased biological activities
; TITLE OF INVENTION: increased biological activities
; TITLE OF INVENTION: increased biological activities
; CURRENT APPLICATION NUMBER: US/09/968,362
; PRIOR PILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NOS: 28
; SEQ ID NO 22
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97.1%; Score 570; DB 16; Length 447;
Best Local Similarity 97.3%; Pred. No. 3.9e-47;
Matches 107; Conservative 1; Mismatches 2; Indels (
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Pred. No. 3.9e-47;
1; Mismatches 2;
             PRIOR APPLICATION NUMBER: US/09/968,362
PRIOR FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 22
LENGTH: 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.3%;
Matches 107; Conservative
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ORGANISM: Artificial Sequence
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US-10-959-318-13
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OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268)
OTHER INFORMATION: mutations
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                                                                                                                                                                                                          APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE COF INVENTION: Polypeptides including modified constant regions
TITLE REFERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: PCT/GB2004/004254
PRIOR PILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: GB0324368.0
PRIOR FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
SEQ ID NO 11
  61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Pred. No. 4.2e-47;
0; Mismatches 1
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                                                                                                     US-10-959-318-11; Sequence 11, Application US/10959318; Publication No. US20050215768A1; GENERAL INFORMATION:
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98.2%;
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ORGANISM: Artificial Seguence
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Best Local Similarity 98.2°
Matches 108; Conservative
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و رو
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OTHER INFORMATION: mutations
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US-10-959-318-8
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                                    GENERAL INFORMATION:
APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE CANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT APPLICATION NUMBER: PCT/GB2004/004254
PRIOR PILING DATE: 2004-110-07
PRIOR FILING DATE: 2004-110-07
PRIOR APPLICATION NUMBER: GB0324368.0
PRIOR PILING DATE: 2003-110-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
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APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REPERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: PCT/GB2004/004254
PRIOR FILING DATE: 2004-10-07
PRIOR PAPLICATION NUMBER: GB0324368.0
PRIOR FILING DATE: 2003-10-17
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llarity 96.4%; Pred. No. 3.8e-47;
Conservative 1; Mismatches 3; Indels (
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Sequence 8, Application US/10959318
Publication No. US20050215768A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.3
SEQ ID NO 8
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ORGANISM: Artificial Sequence
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Best Local Similarity 96.4%;
Matches 106; Conservative
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9

Gaps

1;

DB 18; Length 109; 1; Indels THIS PAGE BLANK (USPTO)

Human IgG Human IgG

Sequence

Sequence Sequence Sequence Rhesus mo Rhesus mo

Variant

Rhesus mo Crab-eati Variant I Variant I

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Human col Camel 1gG Pig 1gG2a Variant I

Llama IgG

ALIGNMENTS

Binding molecule; CH2 sequence; complement dependent lysis; FogammaRIIb; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degramulation; phagocytosis; vasculitis; Crohn's disease; graft-vs-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; sickle cell anaemia; coronary artery occlusion. Ş AAYS4998 standard; protein; 110 Mutated CH2 sequence Gldeltaac. (first entry) 17-FEB-2000 RESULT 1 AAY54998

18-NOV-1999.

99WO-GB001441. 07-MAY-1999; (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

98GB-00009951.

08-MAY-1998;

Williamson LM; Clark MR, Armour KL,

WPI; 2000-039075/03.

Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties.

Claim 12; Fig 17; 81pp; English.

and This sequence represents the mutated CH2 molecule Gideltaac, and is a binding molecule of the invention. The recombinant binding molecule is capabble of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; a (b) an effector domain that is homologous to all or part of a constant

1206590

of hits satisfying chosen parameters: 2105692 segs, 386760381 residues

Total number

Searched:

BLOSUM62

Scoring table:

score:

Sequence:

OM protein

Run on:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 110

A_Geneseq_16Dec04:*

Database

geneseqp2000s:* geneseqp2001s:* geneseqp1980s:* geneseqp1990s:*

WO9958572-A1 Synthetic.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:*

rip	Aay54998 Mutated C Aay54996 Mutated C Aay57860 Human imm Aar77800 Human imm Adh75385 Human igd Add25659 Binding d Aar41717 Undefined Aac28089 Human imm Adh75413 CH2 regio Adr57438 OKT3 mono Add257438 OKT3 mono Add25743 Binding d Aar41709 Undefined Aay54997 Mutated C Aay42626 Human igG Aar41713 Undefined Adj52129 CH1 delet Adj52129 CH1 delet Adj52132 CH1 delet Adj52132 CH1 delet Adj52132 CH1 delet Adj52132 CH1 delet Adj52132 CH1 delet Adj52132 CH1 delet Adj52132 CH1 delet Adj52135 CH delet Adj5213 Human imm Aar75349 C Ggamma-1
SUM	AAY54998 AAX54996 AAX41689 AAX41689 AAX41689 AD25659 AD25659 AD25659 AD15515 AD15515 AD175413 AD175413 AAX674109 AAX41709 AAX5497 AAX841713 AD25132 AAX71023 AAX71023 AAX71033
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Result No.	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

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compain of a human immunoglobulin G (IgG) heavy chain. The binding molecule is used to bind a target molecule (especially FogammaRIID cortains inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule is useful for the treatment of graft-verocetic probability of a second binding molecule e.g. an antibody, to the target condecule. The binding molecule is useful for the treatment of graft-verons transplant rejection, bone-marrow transplant rejection, bone-marrow transplant cortain transplant rejection, autoimmune thrombocytopaenia and arthritis, alloimmunity (e.g. vasculitis, autoimmunity (e.g. catoimmune thrombocytopaenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN chronic or acute inflammatory diseases (e.g. Crohn's, HDN chronic or acute inflammatory diseases (e.g. Crohn's, HDN cortain and cortains). Goodpastures, sickle cell anaemia and cortains the corronary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FogammaR and desirable corpoperties have been retained. The polypoptides do not contain nonthuman amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent changed all per presents.
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Pred. No. 1.4e-51;
0; Mismatches 1;
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99.1%;
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Best Local Similarity 99.1
Matches 109; Conservative
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Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin

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This sequence represents the mutated CH2 molecule Gideltaab, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (C) an effector domain that is homologous to all or part of a constant comparing inhibition of B cell activation, mast cell degranulation or the planding molecule (especially FegammaRIID causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the consequence. The binding molecule, e.g. an antibody, to the target consequence or activate in the binding molecule is useful for the treatment of graft-vs. The binding molecule is useful for the treatment of graft-vs. The binding molecule is useful for the treatment of graft-vs. The binding molecule is useful for the treatment of graft-vs. The binding molecule is useful for the treatment of graft-vs. The binding molecule and arthritis), alloimmunity (e.g. concent) autoimmunity (e.g. concent) autoimmunity (e.g. crohn's, HDN chronic or acute inflammatory diseases (e.g. Crohn's, HDN coronary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FegammaR and desirable thuman amino acids, and are therefore likely to have reduced immunogeniciby. Further, they still bind Protein A, which is consistent contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and contain and 
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Pred. No. 5.3e-51;
0; Mismatches 0;
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                                          Claim 12; Fig 17; 81pp; English.
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  properties.
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gene. The vector also includes a heavy chain immunoglobulin enhancer and the human gammal constant region (CH). The VH region of 128.1 was 1901ated by polymerase chain reaction and cloned into plasmid pAH4274. This was achieved by digesting the plasmid and the product with Ecogy and NheI. The VH gene was inserted in-frame with the human gammal CH region CH at the 3' end of the VH-J region by means of a NheI site. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuro- pharmaceutical or diagnostic agencia disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a new composition comprises a variant of a parent polypeptide having at least a portion of a FC region. The variant mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells more effectively than the parent polypeptide and comprises at least one amino acid modification at position 280 in the autoimmune diseases. The present sequence represents the amino acid sequence of a human immunoglobulin G, IGG, CH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising a variant of a parent polypeptide having least a portion of a Fe region, useful in treating e.g., autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC; autoimmune disease; human; IgG; immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                Score 557; DB 2; Length 110;
Pred. No. 1.3e-49;
                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.36
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH75385 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-2003; 2003US-00370749.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 94.5
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human IgG1 CH2 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watkins JD, Allan B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-070755/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WATK/) WATKINS J D. (ALLA/) ALLAN B.
                                                                                                                                                                                                                                                                                                                                      Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2004002587-A1
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ADH75385
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                                                                                                                                                            In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17. The inventor's propose eliminating these allotypes by amino acid changes to agree with the sequences of IgG2, IgG3 and IgG4. None of the allotype sites (1, 2 and 17) are located within the CH2 domain. New "isoallotypes" should be suitable for therapeutic use in all patients. See AAR27678-R27681. (Updated on 25-MAR-2003 to correct PN field.)
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                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light; chain; variable; constant; region; anti-human; transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                             - useful causing
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                          Humanised antibodies having modified allotypic determinant matching allotypes in therapy with decreased likelihood of
                                                                                                                                                                                                                                                                                                                                                                                Length 110;
                                                                                                                                                                                                                                                                                                                                                                           94.9%; Score 557; DB 2; Length 11
94.5%; Pred. No. 1.3e-49;
ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 11K; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR41684 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Undefined ORF2 encoded by pAH4602.
                                                                                                                  Disclosure, Fig 4c; 57pp; English.
                                                                      undesirable immune responses.
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Best Local Similarity 94.5
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-196742/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ43844.
                                                                                                                                                                                                                                                                                                                                 Sequence 110 AA;
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20-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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24-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide that is fused to the CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide or the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one
                                                                                                                                                                                                                                                                                                                                                                                         Binding domain, immunoglobulin, fusion protein, cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region, 1gG1, antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent cell-fiscorial cytotoxicity; ADCC; complement fixation; antignate condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myaethenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
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                                                                                                                                  1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                      1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                               Binding domain-immunoglobulin fusion protein-associated protein #107.
                                                                         Gaps
                                                                                                                                                                PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                           PREEDYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                          Length 110;
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                                          Score 557; DB 8;
Pred. No. 1.3e-49;
                                          Query Match
94.9%; Score 557; DE
Best Local Similarity 94.5%; Pred. No. 1.3e
Matches 104; Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                        ADD25659 standard; protein; 109
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03-JUN-2002; 2002US-0385691P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L7-JAN-2001; 2001US-0367358P.
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              Sequence 110 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
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cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunological activity comprising antibody capendent cell-mediated cytocoxicity (ADCC) and complement fixation. The binding domain polypeptide is capable of specifically binding to an antigen. Also included are an isolated polymucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the polymucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a construct, producing the binding domain-immunoglobulin clusion protein or a broad construct, producing the binding domain-immunoglobulin fusion protein suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, cultimunoglobulin fusion protein-associated protein sequence is a binding domain-immunoglobulin fusion protein-associated protein sequence is a binding domain companding protein-associated protein sequence. The sequence data for this patent formed part of the printed specification can disting a subject the sequence. The present sequence in the printed specification by their SEQ ID cumber therefore none of the sequences can be explicitly identified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 3.4e-49;
2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 103; Conservative
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The sequences given in AAR41715-18 are encoded by the expression vector pAH4808. This vector represents the cloning of the human gamma isotype, gamma-4, with the variable region of the murine monoclonal antibody (18.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CHI, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones were isolated. Is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent or diagnostic agent. The conjugate may also be used for diagnostic gentuclogical disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzhaimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma globulinaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia; vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial; immunosuppressive; lymphoid malignancy; respiratory syncytial virus; anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APEFLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                  Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 110;
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                                                                                                                             Disclosure, Fig 19J; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE28089 standard; protein; 109 AA
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                 WPI; 1993-196742/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 110 AA;
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Matches
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Ward ES;

Dall'acqua W, Johnson LS,

WPI; 2002-666925/71.

(MEDI-) MEDIMMUNE INC

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                                                                                                                    an IgG constant domain having at least one amino acid modification. The immunoglobulins are used in the treatment or prevention of a disease or disorder by passive immunotherapy for vaccinating a subject and for in vivo diagnosis of a subject. The disease and disorders include a gamma globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versusthest, lymphoid malignancies and passive immunotherapies and also for the treatment of various systemic infections. The present sequence is human immunoglobuling (IgG1) Fc region second constant (FR2) domain
                                                                                                           The invention relates to a modified immunoglobulin (IgG1) which comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the
                                                                                                                                                                                                                                                                                                                                                                                                                 1 APELLGGPSVFLFPPFKPKDTLMISRTPEVTCVVVDVSHBDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a new composition comprises a variant of a parent polypeptide having at least a portion of a Fc region. The variant mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells more effectively than the parent polypeptide and comprises at least one amino acid modification at position 280 in the Fc region. The composition is useful in treating diseases e.g.,
Modified immunoglobulins useful in the treatment of autoimmune diseases, comprises at least one amino acid modification relative to a wild-type immunoglobulin constant domain.
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                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody-dependent cell-mediated cytotoxicity; ADCC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109
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                                                                                                                                                                                                                                                                                                                        Length 109;
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                                                                                                                                                                                                                                                                                                                      ; DB 5;
4.3e-49;
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; Pred. No. 4.3e-
2; Mismatches
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                                                                        Disclosure; Page 138; 147pp; English.
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                                                                                                                                                                                                                                                                                                                      94.0%;
94.5%;
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 94.5
Matches 103; Conservative
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(ALLA/) ALLAN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watkins JD, Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disease
                                                                                                                                                                                                                                                                                       Sequence 109 AA;
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25-MAR-2003 (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for generating an immune response to an antigen in a patient. The method comprises administering to the patient an immunoglobulin (Ig) or its portion where the Ig has at least one peptide epitope of the antigen attached to the Ig or its portion and administering the immunoglobulin or its portion in conjunction with a RNA segment. A recombinant human Ig molecule capable of binding to an FC gamma receptor (FcgammaR) of an antigen presenting cell (APC) was used to illustrate the invention. The recombinant human Ig molecule comprises a CH3 region (ADL90102), a CH2 region (ADL90103), a hinge region (ADL90104) and a flanking peptide (ADL90105).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generating an immune response to an antigen, useful for generating desired T cell responses comprises administering an immunoglobulin having one peptide epitope of the antigen attached to the immunoglobulin.
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                                                                                                                                                Gaps
autoimmune diseases. The present sequence represents a CH2 region
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                                                                                                                                              Indels
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                                                                                        Score 552; DB 8; Le
Pred. No. 4.4e-49;
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                                                                                                                                              2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                             ADL90103 standard; protein; 110
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14-MAR-2003; 2003WO-US007995.
                                                                                                   Query Match
Best Local Similarity 93.6%;
Matches 103; Conservative
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Best Local Similarity
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                                                              Sequence 110 AA;
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Matches 103,
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The invention relates to a new composition comprises a variant of a parent polypeptide having at least a portion of a FC region. The variant mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells more effectively than the parent polypeptide and comprises at least one amino acid medification at position 280 in the FC region. The composition is useful in treating diseases e.g., autoimmune diseases. The present sequence represents a CH2 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVHGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising a variant of a parent polypeptide having at least a portion of a Fe region, useful in treating e.g., autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGGESVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVFNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                       Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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Pred. No. 7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 51; 62pp; English
                                                                                                                                                                             ADH75413 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-2003; 2003US-00370749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-2002; 2002US-0358161P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.7%;
                                                                                                                                                                                                                                                                                                   22-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                CH2 region D280H variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-070755/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WATK/) WATKINS J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Thompson PA;

us-09-674-857-3.LL.rag

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New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 322; 157pp; English.
                                                                                                                                                           Ledbetter JA, Hayden-Ledbetter MS,
                                                                                  17-JAN-2001; 2001US-0367358P.
17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
                                                            25-JUL-2002; 2002US-00207655
                                                                                                                                  (GENE-) GENECRAFT INC
                                                                                                                                                                                  WPI; 2003-801317/75.
                                     26-JUN-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; andignant condition; Becal disorder; melanoma; cardinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                               cell activating and immunosuppressive activity, and is used to treat transplant patients to prevent rejection. The antibody can be engineered to contain a human Fc region. By transferring the binding specificity into a human framework, the immunoganicity is reduced without affecting the immunosuppressive activity. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                           New humanised OKT3 antibody with mutated Fc receptor binding region - useful as immunosuppressant to reduce transplant rejection, lacks the T-cell activating side effects of wild type antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                   The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) has potent T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binding domain-immunoglobulin fusion protein-associated protein #149.
                                              OKT3; monoclonal antibody; antibody engineering; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Binding domain, immunoglobulin; fusion protein; cytostatic;
antiarthitic; immunosuppressive; antidiabetic; antithyroid;
neuroprotective; hinge region; immunoglobulin heavy chain;
CH2 constant region; CH3 constant region; 1gG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.5%; Score 549; DB 2; 94.5%; Pred. No. 8.8e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 82-87; 135pp; English
                                                                                                                                                                                                                                 Jolliffe L:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD25761 standard; protein; 109 AA
                        OKT3 monoclonal antibody fragment.
                                                                                                                                                          94WO-US006198
                                                                                                                                                                                 93US-00070116
(first entry)
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                                                                                                                                                                                                                                 Bluestone JA, Zivin RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                       (ARCH-) ARCH DEV CORP
                                                                                                                                                                                                                                                        WPI; 1995-022721/03.
                                                            numanized antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                   P-PSDB; AAQ75356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 109 AA;
                                                                                   Mus musculus
                                                                                                          WO9428027-A1
                                                                                                                                                         01-JUN-1994;
                                                                                                                                                                                 01-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                  38-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Simi
Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                          ield.)
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The inventorial relaters to a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide. The constant region polypeptide comprises: a wild-type human igdi immunoglobulin hinge region polypeptide comprises: a wild-type human igdi immunoglobulin hinge region polypeptide; derived from (a) having 3 or more cysteine residues; where the first cysteine is not mutated; a mutated human igdi immunoglobulin hinge region polypeptide contains 2 cysteine residues; where the first cysteine is not mutated; a mutated human igdi immunoglobulin hinge region polypeptide contains or more cysteine residues; where the mutated human igdi immunoglobulin hinge region polypeptide contains no more than one cysteine residue; mutated human igdi immunoglobulin hinge region polypeptide contains no cysteine residues; may having 3 or more cysteine residues; where the mutated human igdi immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains on cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains construct construct least one immunological activity comprising the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polymuclectide (operably linked to a promoter) construct comprising the polymuclectide (operably linked to a promoter) and a host for a most construct comprising the polymuclectide (operably linked to a promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein a subject thaving a mailgnant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject baving or suspected of having a mailgnant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein-sar comman, rheumatoid arthritis, mysthenia gravis, Grave's disease, type I diabetes mellitus, multiple calerosis or autoimmune disease. The present sequence is a binding domain immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at sequence data for this patent formed part of the printed specification is also available in electronic format directly from USPTO at sequence the sequence in the printed specification by their SBO ID common therefore none of the sequences can be explicitly identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
The invention relates to a binding domain-immunoglobulin fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 93.6
Matches 102, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 109 AA;
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The sequences given in AAR41707-09 are encoded by the expression vector pAH4625. This vector represents the cloning of the human gamma isotype, gamma-2, with the variable region of the murine monoclonal antibody is gamma-2, with the variable region of the murine monoclonal antibody in which heavy chain (VH) is derived from a murine source and the sequences encoding CHI, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector page 180 AAQ43845), was transfected into SP2/0 cells and clones were isolated. Is an anti-human transferrin receptor antibody which binds to the transferrin receptor antibody which binds to the transferrin receptor antibody which binds to the transferrin receptor antibody which binds to the cransferrin receptor antibody which binds to the transferrin disorders in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eq. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzhaimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                     Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; diagnostic; agent; tumour; AlDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders.
                   61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.6%; Score 543.5; DB 2; Best Local Similarity 92.7%; Pred. No. 3.3e-48; Matches 102; Conservative 5; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                               Undefined ORF2 encoded by plasmid pAH4625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 17J; 151pp; English
                                                                                                                                               Ą.
                                                                                                                                           AAR41709 standard; protein; 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92WO-US010206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-00800458
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ALKE-) ALKERMES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-196742/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ43846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9310819-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-NOV-1992;
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                                                                                                                                                                                                                               25-MAR-2003
20-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Friden PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                       AAR41709;
                                                                                                     RESULT 14
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This sequence represents the mutated CH2 molecule G2deltaa, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and comprises: (a) a binding domain capable of binding a target molecule; and compain of a human immunoglobulin G (IgG) heavy chain. The binding constant domain of a human immunoglobulin G (IgG) heavy chain. The binding constant consists in the binding molecule can be used to prevent or inhibit the consists in the binding molecule can be used to prevent or inhibit the consists in the binding molecule can be used to prevent or inhibit the consists in the binding molecule is useful for the treatment of graft-vs-consists or actorimmunity (e.g. vascultis), autoimmune haramplant rejection, bone-marrow transplant correction, bone-marrow transplant correction autoimmune haramplants (e.g. crohn's, HDN chroblastosis foetalis), Goodpastures, sickle cell anaemia and correctivate inflammatory diseases (e.g. Crohn's, HDN corromary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through Fegammas and desirable complement or trigger cytotoxic activities through Fegammas and desirable human amino acids, and are therefore likely to have reduced human amino acids, and are therefore likely how are decembled.
                                                                                                                                                                                                                                                                                                  Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIID; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-vs-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; encenatal alloimmune thrombocytopaenia; Goodpastures disease; therapy; sickle cell anaemia; coronary artery occlusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenicity. Further, they still bind Protein A, which is consistent with being able to cross the human placenta through interaction with FCRn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulic-derived binding molecules that do not activate complement
or trigger cytotoxic activities and maintaining desirable immunoglobulin
(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williamson LM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Fig 17; 81pp; English.
                                                                                                                                 AAY54997 standard; protein; 109
                                                                                                                                                                                                                                                                Mutated CH2 sequence G2deltaa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-GB001441.
                                                                                                                                                                                                                     17-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-039075/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9958572-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Armour KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                    RESULT 1
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Sequence 109 AA;

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1; Gaps

Indels

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61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110

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Query Match 92.6%; Score 543.5; DB 3; Length 109; Best Local Similarity 93.6%; Pred. No. 3.3e-48; Matches 103; Conservative 4; Mismatches 2; Indels 1; Gaps
                                                                                                     Search completed: November 17, 2005, 07:47:00 Job time: 89.9087 secs
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November 17, 2005, 07:37:49; Search time 16.5753 Seconds (without alignments) 638.529 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                        Run on:
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US-09-674-857-3 587 1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110 44790 Total number of hits satisfying chosen parameters: ~ 283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Perfect score: Sequence: Scoring table: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 110

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Iq qamma-2b chain	IdE chain C3 regio	IgE chain C3 regio	Ig kappa chain Cr	Ig lambda chain C	Ig upsilon chain -	Ig lambda chain C	Ig lambda-5 chain		Ig lambda-1 chain	Ig lambda-5 chain	Ig lambda-2 chain										Ig lambda chain C				Iq lambda chain C	Ig kappa-2 chain C		Ig lambda-2 chain
SUMMAKIES	ID	A30503	168726	168730	кзни	B26167	S43147	B30554	B26434	S26653	LIMS	800259	S22760	F53275	A37927	B34509	H32529	K4RB	150741	150740	L2HU	S26654	L7RB	KSRBV	KIMS	A27390	L1PG	K4RBBS	G20907	B27390
	1 DB	2	2	2	•	3	•		2	2	H	7	2	7	2	~	~	-	7	7	•	2	7	-		7		-	7	7
	Lengt	8	10.	107	10	10.	11(101	101	9,	10	10(10(107	9,	107	10.	10	106	106	105	5	10,	10	106	10	105	106	106	105
æ	Query Match Length DB	47.0	24.0	23.5	22.3	22.1	22.0	21.7	21.6	21.5	20.7	20.7	20.7	19.8	19.6	19.4	19.3	19.1	18.7	18.7	18.7	18.5	18.5	17.7	17.5	17.2	17.0	16.8	16.8	16.2
	Score	276	141	138	131	130	129	127.5	126.5	126	121.5	121.5	121.5	116	115	114	113.5	112	110	110	109.5	108.5	108.5	104	103	101	99.5	98.5	98.5	95
	Result No.	-4	8	٣	4	ς,	9	7	80	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig kappa chain C r	lambda-chain C-req	Ig kappa-B9 chain	Ig kappa-B5 chain	Ig lambda-3 chain		Ig kappa chain C r	Ig gamma-1 chain C	Ig light chain C r	Ig lambda2-like ch	Ig light chain C r	Ig gamma-3 chain C	Ig lambda chain, C	Ig lambda-2 chain	Ig lambda-2 chain	IgE chain C2 regio	
KIRTB	146731	K9RB	KSRB	L3MS	S22762	KIRTA	S26652	C34509	157802	D34509	A24629	PL0186	LZMS	S22759	168725	
Н	~	Н	٦	٦	7	н	~	N	~	~	7	7	-	~	~	
106	102	104	103	104	105	106	97	78	82	78	06	67	104	105	107	
16.2	15.9	15.8	15.7	15.3	15.3	15.3	14.5	14.2	13.6	13.5	13.5	13.0	12.9	12.9	11.0	
95	93.5	92.5	92	90	90	90	82	83.5	80	79.5	79	76.5	76	16	64.5	٠
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1 RESULT 1 RESULT 2 RESULT 3 RESULT 3 RESULT 3 RESULT 4 RESULT 4 RESULT 4 RESULT 5 RESULT 5 RESULT 5 RESULT 6 RESULT 6 RESULT 7 RESULT 8 RESULT 8 RESULT 8 RESULT 8 RESULT 8 RESULT 8 RESULT 7 RESULT 8 RESULT 9 RESULT 8 RESULT 9 RESULT 9 RESULT 9 RESULT 9 RESULT 9 RESULT 8 RESULT 9 RESULT 9 RESULT 9 RESULT 9 RESULT 9 RESULT 9 RESULT 8 RESULT 8 RESULT 8 RESULT 9 RESULT 9 RESULT 8 RESULT 9 RESULT	A; Cross-references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460	Comparison of the comparison o
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Thu Nov 17

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Riffleter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P. 6-611 22, 197-207, 1980
6-611 22, 197-207, 1980
A;Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserv
A;Reference number: A90806; MUID:81042304; PMID:6775818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A;Reference number: S02572; MUID:88005152; PMID:3115831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Map position: 2p12-2p12

C,Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kay can immunoglobulin heterotetramer subunit subunits associate into 1: C,Superfamily: immunoglobulin C region; immunoglobulin homology

C,Superfamily: immunoglobulin C region; immunoglobulin homology

E,19-88/Domain: immunoglobulin homology < IMM>

F,26-86/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ajmolecule type: protein
Ajmolecule type: protein
Ajmolecule type: protein
Ajmolecule type: protein
Ajmolecule type: protein
Ajmolecule type: protein
Ajmolecule type: protein the Inv (1,2) allotypic marker, 45-Ala and 83-Leu
Rjillachmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
AjTille: Die volstaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).
Ajmille: Die volstaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).
AjContents: Bence Jones protein Cum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 1-56, 'Q', 58-106 <HI2>
A; Residues: 1-56, 'Q', 58-106 <HI2>
A; Titani, K.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 244, 3550-3560, 1969
A; Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete A; Reference number: A92047; MUID: 69234734; PMID: 4893682
A; Contents: Bence Jones protein Ag
                                                                                                                                                                                                                                                                                 A;Cross-references: GB:J00241; NID:g33140; PIDN:CAA23823.1; PID:g1335148
A;Note: the sequence was determined from the germline gene
R;Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: A92047
A;Molecule type: protein
A;Reaidues: 1-13,'N',15-106 <TIT>
A;Reaidues: 1-13,'N',15-106 <TIT>
Science 169, 56-59, 1970
A;Title: Macroglobulin structure: variable sequence of light and heavy chains.
A;Accession: A94242; MUID:70201507; PMID:5447531
A;Accession: A94242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV--EVHNAKTKPREEQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;106/Disulfide bonds: interchain (to heavy chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Readues: 1-13, N', 15-106 < KOH>
A; Readues: 1-13, N', 15-106 < KOH>
A; Readues: 1-13, N', 15-106 < KOH>
A; Richth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, Am. J. Hum. Genet. 48, 613-620, 1991
A; Title: Km typing with PCR: application to population screening.
A; Reference number: A37927; MUID:91150772; PMID:1900145
A; Accession: B37927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.3%; Score 131; DB
30.5%; Pred. No. 6e-0
tive 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GDB:120088; OMIM:147200
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A94417
A;Contents: Bence Jones protein Roy
A;Accession: A94417
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Best Local Similarity 30.5*
Matches 32; Conservative
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R,Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-106 <HIE>
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A; Residues: 8-106 < KUR>
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R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid A;Reference number: 154443; MuID:88152907; PMID:3346043
A;Accession: 168730
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                               7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IgE chain C3 region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 GVITYLIPPSPLD-LYQNGAPKLTCLVVDLESEKNVNVTWNQEKKTSVSASQWY---TKH
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ajmolecule type: mRNA
AjResidues: 1-107 «RES»
Ajresidues: 1-107 «RES»
Ajresidues: 1-107 «RES»
Cysuperfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology «IMM»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
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    Length 107;
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                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                         64 NATTSITELPVVAKDWIEGYGYQCIVDHPDFPKPIVRSITK 10S
                                                                                                                                                                                                                                                                                                                               67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK 108
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24.0%; Score 141; DB 2; 31.4%; Pred. No. 6.2e-07; ive 21; Mismatches 47
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                                     Best Local Similarity 31.44
Matches 32; Conservative
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Best Local Similarity
Matches 35; Conserv
        Query Match
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L.L

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Gaps

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Ig lambda-5 chain C region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1988 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
C;Accession: B26434
R;Saksguchi, N.; Melchers, F.
Rsture 324, 579-582, 1986
A;Title: Lambda-5, a new light-chain-related locus selectively expressed in pre-B lymph:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: S26653 ... Harfeldt, K.E.; Isaacson, C.; Oestberg, L. K; Ehrlich, P.H.; Moustafa, 2.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L. Hum. Antibodies Hybridomas 1, 23-26, 1990 ... A;Title: Potential of primate monoclonal antibodies to substitute for human antibodies: A;Reference number: S26652; MUID:91355693; PMID:2129418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH-NAKTKPREEQY 66
   C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Dacte: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C;Accession: B30554
Immunol. 142, 708-711, 1989
A;Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A;Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A;Reference number: A30554; MUID:89093962; PMID:2492052
A;Accession: B30554
A;Molecule type: mRNA
A;Residues: preliminary; not compared with conceptual translation
A;Residues: 1-105 *FOLD.
A;Accession: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSVTLFPPSKEE--LDTNKATVVČLISD--FYPGSVNVVWKADGSIINQNVKTTQASKÓS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:MJ0387
A;Note: the authors translated the codon TAC for residue 84 as Thr
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 127.5; DB 2
Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.7%; Sco...
30.8%; Pred. No. 1...
"'ve 21; Mismatches
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A;Molecule type: mRNA
A;Residues: 1-99 <EHR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 30.8*
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-105 <SAK>
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A; Reference number: A26167
A; Rocession: B26167
A; Rocelcule type: mRNA; DNA
A; Residues: 1-103 < PAR>
A; Residues: 1-103 < PAR>
A; Residues: 1-103 < PAR>
A; Cross-references: UNIPROT:P20763; GB:M33049
A; Cross-references: UNIPROT:P20763; GB:M33049
C; Superfamily: immunoglobulin cone cDNA clone
C; Superfamily: immunoglobulin immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 21-87/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Anas platyrhynchos (domestic duck)
C;Species: Anas platyrhynchos (domestic duck)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
R;Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
B;Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
A;Description: Evidence from duck immunoglobulin genes that IgY is the common ancestor of A;Accession: 843145
A;Accession: 843147
A;Status: preliminary
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R; Parvari, R.; Ziv, E.; Lentner, F.; Tel-Or, S.; Burstein, Y.; Schechter, I.
EMBO J. 6, 97-102, 1987
                                                                                                                                                                                                                                                                                                                       Ig lambda chain C region - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 PQRQSNSQYMASSYLSLSASDWSSHETYTCRVTHNG--TSITKTLKRSE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 110;
                                                                                                 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                            Length 103
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A;Residues: 1-110 cMAG.
A;Cross-references: EMBL:X78355; NID:g468612; PID:g468613
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Indels
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FTASSSLAISTODWLAGERFICTVOHEDLPEPLGKSIAK 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.1%; Score 130; DB 2; Best Local Similarity 31.2%; Pred. No. 7.2e-06; Matches 34; Conservative 25; Mismatches 42
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B30554
Ig lambda chain C region - sheep (fragment)
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A;Cross-references: UNIPROT:Q9D8W4; EMBL:X58411; NID:g51763; PIDN:CAA41312.1; PID:g51764 (S.Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iglands-2 chain C region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: S22760
R;Weiss, S.; Wu, G.E.
BMBO J. 6, 927-992, 1987
A;Title: Somatic point mutations in unrearranged immunoglobulin gene segments encoding A;Reference number: S22759; WUD:87246527; PMID:3109891
                                          7 PLVTLFLPSLKNL---QANKVTLVCLVSEFYPGTLVVDWKVDGVPVTQGVETTQPSKQT 62
                                                                                                                                                                                                                                                                                                                                            Ig lambda-5 chain C region - western wild mouse C;Species: Mus spretus (western wild mouse) C;Date: 31-Dec-1988 #sequence_revision 07-Sep-1990 #text_change 21-Jan-2000 C;Accession: S00259 R;Mami, F.; Cazenave, P.A.; Kindt, T.J. BMBO J. 7, 117-122, 1988 A;Title: Conservation of the immunoglobulin C-lambda-5 gene in the Mus genus. A;Reference number: S00259; MuID:88196070; PMID:3129289
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPREEQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                         67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.7%; Score 121.5; DB 2
30.8%; Pred. No. 5.2e-05;
live 22; Mismatches 43
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Best Local Similarity 30.8*
Matches 32; Conservative
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Matches 32;
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                                                                                                                                                                                                                                                                                 8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV--EVHNAKTKPREEQ 65
                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig lambda-1 chain C region - mouse
C;Species: Mus musculus (house mouse)
C;Dacesia: 31-Mar-1981 #sequence_revision 29-Jun-1981 #text_change 09-Jul-2004
C;Accession: A93922; A93251; A93282; A93775; A02126
R;Selsing, B.; Miller, J.; Wilson, R.; Storb, U.
Proc. Natl. Acad. Sci. U.S. A. 79, 4681-4685, 1982
A;Fitle: Evolution of mouse immunoglobulin lambda genes.
A;Reference number: A93922; MUID:83014953; PMID:6812053
                                                                                                                                                                                                                                                                                                                        Gaps
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                             Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                       Length 99;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                          66 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
                                                                                                                                                       Query Match 21.5%; Score 126; DB 2; Best Local Similarity 32.3%; Pred. No. 1.7e-05; Matches 32; Conservative 20; Mismatches 41.
A)Cross-reterence.
C;Superfamily: immunoglobulin C region; immunoglobulin
F;19-88/Domain: immunoglobulin homology <IMM>
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86

Length 102; 41; Indels

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8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG-VEVHNAKTKPREEQY
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A, Residues: 1-102 <SCH>
A, Cross-references: GB:M29044; NID:g212941; PIDN:AAA49153.1; PID:g212942
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: immunoglobulin
A; Reference number: A34509; MUID: 90099382; PMID: 2513577
                                                                                                                                                                                                                                                                                                                                                               Query Match
19.4%; Score 114; DB 2;
Best Local Similarity 31.5%; Pred. No. 0.00027;
Matches 29; Conservative 18; Mismatches 41
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                                          A; Accession: B34509
A; Status: preliminary
                                                                                                                            A; Molecule type: mRNA
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C;Species: Carcharhinus plumbeus (sandbar shark)
C;Date: 22-Unn-1990 #sequence_revision 22-Unn-1990 #text_change 17-Nov-2000
C;Accession: B34509
R;Schluter, S.F.; Hohman, V.S.; Edmundson, A.B.; Marchalonis, J.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 9961-9965, 1989
A;Title: Evolution of immunoglobulin light chains: cDNA clones specifying sandbar shark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV--EVHNAKTKPREEQYNS 68
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                                                                    ig Kappa-1 chain C region b95 allotype - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Dacies: Oryctolagus cuniculus (domestic rabbit)
C;Dacession: F53275
R;Ayadi, H.; Marche, P.N.; Cazenave, P.A.
Immunogenetics 34, 201-207, 1991
A;Title: Evolution of the rabbit immunoglobulin kappa chain genes.
A;Accession: F53275
A;Accession: F53275
A;Accession: F53275
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Ig kappa chain C region (allotype Inv(1,2)) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 21-Jan-2000
C; Accession: A3792;
Am. J. Hum. Genet. 48, 613-620, 1991
A; Title: Km typing with PCR: application to population screening.
A; Reference number: A37927; MUID: 91150772; PMID: 1900145
A; Reference number: A37927
A; Residues: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-99 kKUR>
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 12-81/Domain: immunoglobulin homology < IMM>
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A,Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBIP:56170)
C,Superfamily: immunoglobulin C region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;19-87/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 29.1%,
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GenCore version 5.1.6
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November 17, 2005, 07:13:34; Search time 77.8539 Seconds (without alignments) 723.518 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-674-857-3 587 1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110 Title: Perfect score: Sequence:

1612378 segs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

301588 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 110

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P01834 homo sapien	P20763 gallus gall	P01843 mus musculu	P20765 mus spretus	P20764 mus musculu					P03984 oryctolagus	P01837 mus musculu		P01846 sus scrofa	P01839 oryctolagus				P01841 oryctolagus	P01845 mus musculu	P01836 rattus norv	P01844 mus musculu	_	_	Q6ezi5 bacillus an	Q7xzf9 oryza sativ	Q61bv9 mus musculu	Q61bw2 mus musculu	Q9jkp1 marmota mon		-	Q8fby4 escherichia
SUMMAKIES	ID	KAC HUMAN	LAC CHICK	LACI MOUSE	LACS_MUSSP	LACS MOUSE	Q8TCJS	KAC4_RABIT	LAC_HUMAN	LAC_RABIT	KAC6_RABIT	KAC_MOUSE	LACI_RAT	LAC PIG	KACE RABIT	LAC2_RAT	KACB_RAT	KAC9_RABIT	KAC5_RABIT	LAC3_MOUSE	KACA_RAT	LAC2_MOUSE	Q99J <u>C</u> 1	Q8KYI0	Q6EZI5	Q7XZF9	Q6LBV9	Q6LBW2	Q9JKP1	P79659	P79660	Q8FBY4
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de	Query Match	22.3	22.1	20.7	20.7	20.0	19.2	19.1	18.7	18.5	17.7	17.5	17.2	17.0	16.8	16.2		15.8	15.7	15.3	15.3	٠.	12.9	11.2	11.2	10.7	10.6	10.5	10.4	10.3	10.3	10.2
	Score	131	130	121.5	121.5	117.5	112.5	112	109.5	108.5	104	103	101	99.5	98.5	95	95	92.5	92	90	90	92	9/	99	99	63	62	61.5	61	•	0	09
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P80697 homo sapien Q31248 peromyscus Q3158 mus musculu Q766% uncultured O19472 mus musculu Q9408 mus musculu Q9408 sus scrofa Q8656 mus musculu Q3151 attus norv Q766% uncultured P13123 sulfolobus Q26127 trypanosoma Q97116 sulfolobus
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                                                         MEDLINE=69234734; PubMed=4893682;
Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";
                                                                                                                                                                                                                                                             Olsen K.E., Sletter K., Westermark P.;
"Extended analysis of AL-amyloid protein from abdominal wall subcutaneous far blopsy: kappa IV immunoglobulin light chain.";
Blochem. Blophys. Res. Commun. 245:713-716(1998).
-!- MISCELLANBOUS: The EU sequence has the INV (3) allotypic marker, Ala-45 and Val-83. The ROY sequence has the INV (1,2) allotypic marker, Ala-45 and Leu-83.
complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR00110; Ig-like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
PROSITE; PS508236; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
3D-structure; Direct_protein sequencing; Immunoglobulin C region;
                                                                                                                                     SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
MEDLLINE=70201507; PubMed=5447531;
KOhler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interchain (with a heavy chain). V -> L (in INV(1,2) marker). FITIG-VAR_003997. D -> N (in Ref. 7 and 8). E -> Q (in Ref. 5 and 6).
                                                                                                                                                                                                                                      TISSUE-Abdominal adipose tissue;
MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
                       Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig-like.
                                                                                                             J. Biol. Chem. 244:3550-3560(1969)
                                                                                                                                                                                                                            SEQUENCE OF 1-33; 38-41 AND 62-80.
                                                SEQUENCE (BENCE-JONES PROTEIN AG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 1D5B; X-ray; A/L=1-103.
PDB; 1D5B; X-ray; L=1-103.
PDB; 1D6V; X-ray; L=1-103.
PDB; 1HEZ; X-ray; -.
PDB; 1HKZ; X-ray; L=1-106.
PDB; 117Z; X-ray; A/C=1-106.
PDB; 1MIM; X-ray; L=1-105.
Genew; HGNC:5716; IGKC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J00241; AAA58989.1; -.
                                                                                                                                                                                                   Science 169:56-59(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H-InvDB; HIX0021121; -.
MIM; 147200; -.
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86
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106
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                                                                                                                                                                                                                                                                                 5 PSVFIFP--PSDEQLKSGTASVVCLLNNFYPR--EAKVQWKVDNALQSGNSQESVTEQDS 60
                                                                                                                                                                                                                                                               8 PSVFLFPPKPKDTLMISRTPBVTCVVVDVSHBDPEVKFNWYVDGV--EVHNAKTKPREEQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=87218480; PubMed=3107981;
Parvari R., Ziv B., Lentner F., Tel-Or S., Burstein Y., Schechter I.;
"Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germline V lambda genes and allotypes of the C lambda locus.";
EMBO J. 6:97-102(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig lambda chain C region.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                    Gaps
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SMART; SM00407; IGcl; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin C region; Immunoglobulin domain; Polymorphism.
NON_TER
                                                                                                                                                                                                 22.3%; Score 131; DB 1; Length 106; 30.5%; Pred. No. 2.8e-05; ive 24; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                             66 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                         61 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 105
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77BF341B511B91B2 CRC64;
                                                                                                                                                                      11609 MW; 51984D1FDD372CE8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         103 AA
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11361 MW;
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InterPro, IPR007110, Ig-like.
InterPro, IPR003597, Ig_cl.
InterPro, IPR03006; Ig_MHC.
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                                                                                                                                                                                                Query Match
Best Local Similarity 30.5%
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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103 1
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103 AA;
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P20763;
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                                                                                                                                      Appella E.;
'Amino acid sequences of two mouse immunoglobulin lambda chains.";
Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971)
-!- MISCELLANEOUS: The MOPC 315 cell line produces 2 light chains, 1
normal lambda-2 chain and 1 abnormal lambda-1 chain that is
missing a large part of the V region. The C region sequence (shown here) appears completely normal.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                       2 PPVAGGESVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (S43).
MEDLINE-82220143; PubMed-6283385;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variants of murine immunoglobulin lambda light chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=81146806; Pubmed=6259534;
Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
Gefter M.L., Baltimore D.;
"Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
Nature 290:65-67(1981).
                                                               8;
                                                                                                                                                                                               62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                           Length 103;
                                                             42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=83014953; PubMed=6812053; Selaing E., Miller J., Wilson R., Storb U.; Selaing E., Miller J., Wilson R., Storb Oct mouse immunoglobulin lambda genes."; Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
                  Query Match 22.1%; Score 130; DB 1; Best Local Similarity 31.2%; Pred. No. 3.5e-05; Matches 34; Conservative 25; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
19 lambda-1 chain C region.
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MEDLINE=71107854; PubMed=5276767;
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PDB; JJNH; X-ray; A=1-105.
INTERPRO; IPRO07110; Ig-like.
InterPro; IPRO03006; Ig_MHC.
Pfam; PF00047; ig; 1.
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                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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Mami F., Cazenave P.A., Kindt T.J.;
"Conservation of the immunoglobulin C lambda 5 gene in the Mus gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 PSVTLPPPSSEEL----ETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQPSKQS
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
3D-structure; Direct protein sequencing; Immunoglobulin C region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.7%; Score 121.5; DB 1; Length 105; 31.1%; Pred. No. 0.00025; ive 18; Mismatches 46; Indels 7
                                                                                                                                                            chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109
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SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                            Interchain (with heavy
                                                                                                                                                                               ET -> TE (in Ref. 4).

Q -> E (in Ref. 4).

Missing (in Ref. 4).

HS -> MI (in Ref. 4).

S -> SS (in Ref. 4).

E -> Q (in Ref. 4).
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01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10 lambda-5 chain C region.
Mus spretus (Western wild mouse)
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                                                             Immunoglobulin domain.
NON TER 1 1 1
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KAC4 RABIT
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QBTCJS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPREEQY 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 PLVTLPLPSLKNL----OANKVTLVCLVSEPYPGTLVVDWKVDGVPVTQGVETTQPSKQT
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MEDLINE=87065143; PubMed=3024017;
Sakaguchi N., Melchers F.;
"Lambda S, a new light-chain-related locus selectively expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pre-B lymphocytes.";
Nature 324:579-582(1986).
-!- TISSUB SPECIFICITY: Selectively expressed in pre-B lymphocytes.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 ;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.7%; Score 121.5; DB 1; Length 105; Best Local Similarity 30.8%; Pred. No. 0.00025; Matches 32; Conservative 22; Mismatches 43; Indels 7;
                                                                                                                                                                                                                                                                                                                                                    104 104 Interchain (with heavy chain).
105 AA; 11674 MW; AAB417DF68471A17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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PROSITE; PS50835; IGG1; 1.
PROSITE; PS00230; IG MHC; FALSE NEG.
Immunoglobulin C region; Immunoglobulin domain.
NON_TER
                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR00359; Ig_c1.
InterPro; IPR00359; Ig_c1.
InterPro; IPR00306; Ig_MHC.
Pfan, PF00047; ig; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS008295; IG_LIKE; 1.
PROSITE; PS002209; IG_MHC; 1.
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01-FEB-1991 (Rel. 17, Last sequence update)
02-UUL-2004 (Rel. 44, Last annotation update)
IG lambda-5 chain C region.
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  send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                          Ig-like.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                            EMBL; M35582; AAA39152.1; -. HSSP; P01843; 1JNH.
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Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
                                                                                                                                                                                                                                                       6 PLVTLFLPSLKN-LQPTR-PQLVCLVSE--FYPGTLVVDWKVDGVPVTQGVETTQPSKQT
                                                                                                                                                                                                                       8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPREEQY
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                                                                                                                                                                          Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                        Length 105;
                                               104 104 Interchain (with heavy chain)
105 AA; 11678 MW; 1F210915904A86A5 CRC64;
                                                                                                                                                                                                                                                                                                                           67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                        Indela
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
101-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp667J0810 (Fragment).
                                                                                                                                                                        40;
                                                                                                                      / Match 20.0%; Score 117.5; DB 1 Local Similarity 31.7%; Pred. No. 0.00062; les 33; Conservative 24; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
18 Appa-b4 chain C region.
Oryctolagus cuniculus (Rabbit).
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Ig-like.
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PROSITE; PS00290; IG MHC; UNKNOWN_1.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF07654; C1-set; 1.
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Matches 29; Conserv
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myeloma
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                                                                                                                                                                                                                                                                                                                                       MEDLINE-75133568; PubMed=1091650;
Chen K.C.S., Kindt T.J., Krause R.M.;
Primary structure of the L. chain from a rabbit homogeneous antibody
Primary structure arbohydrate in Sequence determination of peptides
from tryptic and peptic digests.";
J. Biol. Chem. 250:3289-3296(1978).
-!- MISCELLANGOUS: This chain was obtained from antibody to the
specific carbohydrate of group C Streptococci and was isolated
from the serum of a single rabbit.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                        MEDLINE=83300036; PubMed=6412231; Emorine L. Dreher K.L., Kindt T.J., Max E.E.; Rabbit immunoglobulin kappa genes: structure of a germline b4 allotype J-C locus and evidence for several b4-related sequences in the rabbit genome."; Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
                                                                                                                                                                                                                        MEDLINE-82060334; PubMed-6795636; Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.; Mucleotide sequence of constant and 3' untranslated regions of a kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit."; Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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PROSITE; PS00815; IG LIKE; 1.
PROSITE; PS00290; IG_WHC; PALSE_NEG.
Direct protein sequencing; Immunoglobulin C region; Immunoglobulin domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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103
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                                                                          SEQUENCE FROM N.A.
                                         NCBI_TaxID=9986;
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STANDARD;

LAC_HUMAN P018423;

RESULT 8
LAC_HUMAN
ID LAC_H
AC P0184

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SEQUENCE (BENCE-JONES PROTEIN SH).
MEDLINE=70166723; PubMed=4909564;
Titani K., Wikler M., Shinoda T., Putnam F.W.;
"The amino acid sequence of a lambda type Bence-Jones protein. 3. The complete amino acid sequence and the location of the disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ponsting1 H., Hess M., Hilschmann N.;
"Structural rule of antibodies. Primary structure of a monoclonal immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-protein Kern). V. The complete amino acid sequence and its genetic interpretation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merlini G., Garver F., Ferri G.; human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
MEDLINE=14109253; PubMed=4814727;
Chen B.L., Poljak R.J.;
"Amino acid sequence, ithe (lambda) light chain of a human myeloma immunoglobulin (IgG New).";
Biochemistry 13:1295-1302(1974).
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
MEDILINE-66088380; Pubmeda-4883841;
Milatein C., Clagg J.B., Jarvis J.M.;
"Immunoglobulin lambda-chains. The complete amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimizu A.; "Comparative studies on the structure of the light chains of human
                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-75046825; PubMed-4215080;
Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           three-dimensional structure of the fab' fragment of a humanoma immunoglobulin at 2.0-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulins. IV. Assignment of a subsubgroup.";
J. Biochem. 93:421-429(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444 (1974)
                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=75013804; PubMed=4415202;
Fett J.W., Deutsch H.F.;
Primary structure of the Mcg lambda chain.";
Biochemistry 13:4102-4114(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE (BENCE-JONES PROTEIN NIG-64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE (BENCE-JONES PROTEIN KERN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stoppini M., Bellotti V., Negri A., "Characterization of the two unique
                                                                                                                                                                                                                                                                                                                                         bridges.";
J. Biol. Chem. 245:2171-2176(1970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Biochem. 228:886-893(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=71150336; PubMed=5549568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE (DOT).
MEDLINE=95255298; PubMed=7737190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=83186114; PubMed=6404900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bence-Jones protein.";
Biochem. J. 110:631-652(1968).
21-JUL-1986 (Rel. 01, Crea
21-JUL-1986 (Rel. 01, Last
25-OCT-2004 (Rel. 45, Last
Ig lambda chain C regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ". suilodolgounmi
                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                       Name=IGLC1;
                                                                                                        Name=IGLC2;
                                                                                                                                          Name=IGLC3;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         Nature 294:536-540(1981).

-!- MISCELLANEOUS: The sequence shown is the Kern-/Oz-/Mcg- chain found in proteins SH, X, and NIG-64. The Kern protein has the Kern+ marker, the NEWM protein has the Oz+ marker, the Mcg protein has the Kern+ marker, and the Mcg+ marker.

-!- MISCELLANEOUS: Six tandem lambda-type genes were identified and the 3 most 5' were sequenced. These correspond to the Mcg sequence (lambda-1), the Kern-/Oz- sequence (lambda-2) and the Kern-/Oz+ sequence (lambda-3).
                                    Edmundson A.B., Ely K.R., Abola E.E., Schiffer M., Panagiotopoulos N., "Rotetional allomeriam and divergent evolution of domains in immunoglobulin light chains." Biochemistry 14:3953-3961 (1975).
                                                                                                                                                                                                                                                                                                             MEDINE-82080680; PubMed-6273747;
Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
"Clustered arrangement of immunoglobulin lambda constant region genes
                                                                                                                                                                                              'n
                                                                                                                                                 MEDLINE=90131913; PubMed=2515285;
Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
Three-dimensional structure of a light chain dimer crystallized
water. Conformational flexibility of a molecule in two crystal
forms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
PROSITE; PS50835; IG LiKE; 1.
PROSITE; PS00290; IG MHC; 1.
3D-Structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin C region; Immunoglobulin C region; Immunoglobulin domain.
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A -> N (in MCG+ marker).
/FIId=VAR 003898.
S -> I (in MCG+ marker).
FTId=VAR 003899.
S -> G (in Ken+ marker).
/FTId=VAR_003900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 1 immunoglobulin-like domain.
                    CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG
                                                                                                                     [10]
K-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF MCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, J00253; AAA59107.1; --
EMBL, L138562, AAB56581.1; ALT INIT.
EMBL, S1754; CAB38569.1; ALT_INIT.
EMBL, X51755; CAA36049.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0003823; F:antigen binding; GO; GO:0006955; P:immune response; InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                        J. Mol. Biol. 210:601-615(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A92057; L2HU.
PDB; 1AQK; X-ray; L21-105.
PDB; 1LLL; X-ray; A/B=1-105.
PDB; ZMCG; X-ray; --
PDB; 7FAB; X-ray; --
Genew; HGNC: 5855; IGLC1.
Genew; HGNC: 5855; IGLC2.
Genew; HGNC: 5856; IGLC2.
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RANGE STATES STA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 PSVTLFPPSSEE--LQANKATLVCLISD--FYPGAVTVAWKADSSPVKAGVETTTPSKQS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxIb=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-82091105, PubMed-6797414; Garcia I., Jaton J.-C.; The primary structure of the constant region of Basilea-rabbit immunoglobulin lambda-chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. J. 197:177-183(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 18.7%; Score 109.5; DB 1; Length 105; Best Local Similarity 27.7%; Pred. No. 0.0039; Matches 28; Conservative 23; Mismatches 43; Indels 7;
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11484 MW; B427513272E8663D CRC64;
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HSSP, P01842; L7RB.
HSSP, P01842; LAQK.
HIGERPRO; LFR003597; Ig_cl.
InterPro; IFR003597; Ig_cl.
InterPro; IFR003597; Ig_mmc.
Ffam; PF00647; Ig_l.
FR081TE; PS00407; IGcl.
FR08ITE; PS00407; IGcl.
InterPro; IFR003597; IGcl.
InterPro; IFR003597; IG_l.
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
T -> K (in MCG+ marker).
/FTId=vAR_003901.
R -> K (in OZ+ marker).
/FTId=vAR_003902.
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01-FFB-1991 (Rel. 17, Last sequence update)
02-JUL-2004 (Rel. 44, Last annotation update)
Ig lambda chain C region
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86
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P01847;
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Pred. No.

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Matches 28; Conserv
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21-JUL-1986 (
25-OCT-2004 (
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P01837;
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                               99
                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emorine L., Sogn J.A., Trinh D., Kindt T.J., Max E.E.;
"A genomic gene encoding the b5 rabbit immunoglobulin kappa constant region: implications for latent allotype phenomenon.";
Proc. Natl. Acad. Sci. U.S.A. 81:1789-1793 (1984).

-!- MISCELLANEOUS: The cDNA from which this sequence was derived contains a terminator codon within the V-region coding region. The origin of this codon and of the differences between this and other sequenced b5 C regions are unclear. The cDNA clone was made using mRNA from trypanosome-infected b5-homozygous rabbits.
                                                PSVILFPPSSEE--LKDNKATLVCLISDFYPR--TVKVNWKADGNSVTQGVDTTQPSKQS
                             8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV-HNAKTKPREEQY
 Gaps
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (CLONE PKB5-F2).
MEDLINE=84041515; PubWed=6314281;
Bernstein K.E., Skurla R.M. Jr., Mage R.G.;
"The sequences of rabbit kappa light chains of b4 and b5 allotypes differ more in their constant regions than in their 3' untranslated
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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A -> VA (in Ref. 2).
7C71850205381751 CRC64;
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                                                                                       67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                          Indels
 47;
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                                                                                                                                                                                                                       23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
23-OT-2005 (Rel. 46, Last annotation update)
Ig kappa chain b5 variant C region.
                                                                                                                                                                                              104 AA
21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 11:7205-7214 (1983)
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EMBL; K01363; AAA31355.1; -.
                                                                                                                                                                                                                                                                                    (Rabbit)
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HSSP, P01837; 25C8.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003006; Ig_MHC.
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Conservative
                                                                                                                                                                                             STANDARD;
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104
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104
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29;
                                                                                                                                                                                             RABIT
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Matches
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8 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG----VEVHNAKTKPRE
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Max B.E., Maizel J.V. Jr., Leder P.;
"The nucleotide sequence of a 5.5-kilobase DNA segment containing the mouse kappa immunoglobulin J and C region genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88329081; PubMed=3138116; de Waele P., Fiers W.; de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.; "Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.; "DNA sequence of the constant gene region of the mouse immunoglobulin
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=82059477; PubMed=6170937;
Hamlinp D.H., Gait M.J., Milstein C.;
Hamlinp D.H., Gait M.D., Milstein C.;
Hompilere sequence of an immunoglobulin mRNA using specific priming and the dideoxynucleotide method of RNA sequencing.";
Nucleic Acids Res. 9:4485-4494(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=79084137; PubMed=103625; DOI=10.1016/0092-8674(78)90290-8; Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.; "Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the dideoxynucleotide method of RNA
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE (MOPC 21).
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Svaati J., Milatein C.;
"The complete amino acid sequence of a mouse kappa light chain.";
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Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Blocchem. J. 126:837-850(1972).
                               12;
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                             Indels
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25-OCT-2004 (Rel. 45, Last annotation update)
Ig kappa chain C region.
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                                Mismatches
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Nucleic Acids Res. 9:971-981(1981)
26.7%; Fr. 24; )
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig_MHC.
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IFSK; X-ray; B/E=1-106.
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                                                                                                                                                                                                                                                                         MEDIJNE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2; Steen M.L., Hellman L., Pettersson U.; "The immunoglobulin lambda locus in rat consists of two C lambda genes and a single V lambda gene.";
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                                                                                                                          Eukaryota, Metazoa, Chodata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus. NCBI_TaxID=10116;
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Washaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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Novocny J., Franek F., Margolies M.N., Haber E.;
Mario acid sequence of normal (microheterogeneous) porcine immunoglobulin lambda chains.";
Biochemistry 16:3765-3772(1977).
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CBF71811F4BC878A CRC64;
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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InterPro; IPR003106; Ig-like.
InterPro; IPR003006; Ig-MHC.
Fam, PP00047; Ig. 1.
SWART; SM00407; IG-li 1.
PROSITE; PS50835; IG-LIKE; 1.
PROSITE; PS50835; IG-LIKE; 1.
Immunoglobulin C region; Immunoglobulin domain.
NOW TER
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 lambda-1 chain C region.
Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 PTVNLFPPSSEEL----GTNKATLVCLISDFYPGAVTVTWKAGGTTVTQGVETTKP-SKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA--KTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANBOUS: In Basilea rabbits, the major type of light chain is lambda. The kappa chain shown is a minor component. All other rabbit B allotypes have Cys-64.
SIMILARITY: Contains 1 immunoglobulin-like domain.
-!- MISCELLANEOUS: This chain was obtained from a mixture of normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Basilea;
PubMed=11894960;
Heidmann O., Rougeon F.;
"Multiplicity of constant kappa light chain genes in the rabbit genome: a b494 homorygous rabbit contains a kappa-bas gene.";
EMBO J. 2:437-441(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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                                                                                                                                                                                                                                                                                                                                                                     104 Interchain (with heavy chain)
11003 MW; 3817AAEBD747C396 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SNNKYAAASSYLALSASDWKSSSGFTCOVTHEG--TIVEKTVTPSE 103
                                             -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                             Direct protein sequencing; Immunoglobulin C region; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 45, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                 Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; V01241; CAA24558.1; -.
EMBL; V00885; -; NOT_ANNOTATED_CDS.
PIR; A02121; K4RBBS.
HSSP, 101837; 25C8.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
                                                          PIR; A02129; LipG.
HSSP; P01842; 2MCG.
HREPPC; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR00306; Ig_MHC.
SPART; SP0047; ig; 1.
SNART; SNO0407; IGCl; 1.
PROSITE; PS00290; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa-b4 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 27.6% les 29; Conservative
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86
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105 AA;
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25-OCT-2004
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steen M.L., Hellman L., Pettersson U.; "The immunoglobulin lambda locus in rat consists of two C lambda genes
                                                                                                                                                                                                                                                                                                                                                                                                                             PVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE-----VHNAK
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 TPQSPE--DNTYSLSSTLSLTSAQYNSHSVYTCEVV-QGSASPIVQSFNR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK 108
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106 AA; 11279 MW; AF9B928DDA853849 CRC64;
                                                                                                                                                                                                                                                                                                         Length 106;
                                                                                                                                                                                                                                                                                                16.8%; Score 98.5; DB 1; Length 10
29.1%; Pred. No. 0.049;
.ive 21; Mismatches 44; Indels
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104 AA; 11318 MW; F087906DE43F7276 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
Pfam; PF00047; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; FALSE_NEG.
Immunoglobulin C regTon; Immunoglobulin domain.
NON TER
DOMĀIN 6 99 Ig-like.
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PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
Immunoglobulin C region; Immunoglobulin domain.
NON TER
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10-OCT-2003 (Rel. 42, Last annotation update)
Ig lambda-2 chain C region.
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HSSP; P01842; 2MCG.
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01-FEB-1991 (Rel. 17, Last seq
10-OCT-2003 (Rel. 42, Last ann
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Gene 55:75-84(1987).
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Interpro; IPR003597; Ig cl.
Interpro; IPR003006; Ig MHC.
Pfam; PF00047; Ig; 1.
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Best Local Similarity 21.44
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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68 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 : | : : | : : | : : | : : | : | : 62 NKYIASSFLRLTAEQWRSRNSFTCQVTHEG--NTVEKSLSPAE 102

Search completed: November 17, 2005, 07:52:17 Job time: 78.8539 secs

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LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
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/cgm2_6/ptodata/1/iaa/BCOMB.pep:*
/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-232-246A-21
US-08-232-246A-44
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US-08-570-116A-4
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US-08-232-246A-30
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US-08-232-246A-38
US-08-232-246A-38
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                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 110
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28 111 22.3 106 2 US-06-796-0344-166 Sequence 166, App 10 111 22.3 106 2 US-06-78-99-40 Sequence 16, App 11 22.3 106 2 US-06-78-99-40 Sequence 26, App 11 22.3 106 2 US-06-78-99-40 Sequence 26, App 11 22.3 106 2 US-06-78-90-50 Sequence 26, App 12 11 22.3 107 1 US-08-444-644.26 Sequence 26, App 13 11 22.3 107 1 US-08-444-644.26 Sequence 26, App 14 22.3 107 1 US-08-442-09-9 Sequence 26, App 15 11 22.3 107 1 US-08-422-09-8 Sequence 26, App 16 17 22.3 107 1 US-08-422-09-8 Sequence 26, App 17 11 22.3 107 2 US-08-90-9 Sequence 26, App 17 11 22.3 107 2 US-08-90-9 Sequence 26, App 17 11 22.3 107 2 US-08-90-9 Sequence 26, App 17 11 22.3 107 2 US-08-90-9 Sequence 26, App 17 11 22.3 107 2 US-08-90-9 Sequence 27, App 18 22.0 108 1 US-08-442-643-8 Sequence 27, App 18 22.0 108 1 US-08-442-643-8 Sequence 27, App 18 22.0 108 1 US-08-444-644-7 Sequence 27, App 18 22.0 108 1 US-08-444-644-7 Sequence 27, App 18 22.0 108 1 US-08-444-684-7 Sequence 27, App 18 22.0 108 2 US-08-444-684-7 Sequence 27, App 18 22.0 108 2 US-08-444-644-7 Sequence 27, App 18 22.0 US-08-444-644-7 Sequence 27, App 18 22.0 US-08-444-644-7 Sequence 27, App 18 22.0 US-08-444-644-7 Sequence 27, App 18 22.0 US-08-444-644-7 Sequence 27, App 18 22.0 US-08-444-644-7 Sequence 27, App 18 22.0 US-08-444-644-7 Sequence 27, App 18 22.0 US-08-444-644-7 Sequence 27, App 18 22.0 US-08-444-644-7 Sequence 27, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 29, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-644-7 Sequence 28, App 18 22.0 US-08-444-6
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1 APELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                   Sequence 44, Application US/08444644

Patent No. 601555
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                          61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                        PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 424
PRIOR PAPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
ATTORNEY AGENT INFORMATION:
NAME: MAGNEY RICHARD W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: PatentIn Policy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 110 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.54
Matches 104; Conservative
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
                                                                                                                                                                                   RESULT 3
US-08-444-644-44
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                                                                        61
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                                                                                                                                                                                                                              1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/08232246A
Patent No. 6329508
GENERAL INFORMATION:
APPLICANT:
Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STRRET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                   1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                             Gaps
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                                                                                                 Length 110;
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                                                                                                                                          4; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/0458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US 07/404,089
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.9%; Score 557; DB 3;
94.5%; Pred. No. 2.1e-58;
tive 2; Mismatches 4;
                                                                                               Score 557; DB 3;
Pred. No. 2.1e-58;
                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REPERENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 861-6240
INFORMATION B61-9540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPE: amino acids
TOPE: amino acids
OLEFIT
                                                                                             Query Match
Best Local Similarity 94.5%;
Matches 104; Conservative
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             protein
internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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    MOLECULE TYPE:
    FRAGMENT TYPE:
US-08-444-644-21
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STATE: MA
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1 APEFLGGPSVPLFPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK Gaps .; 0 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 4; Indels 61 셤

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Houston

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TITLE OF INVENTION: Methods and Materials For Modulation TITLE OF INVENTION: Of the Immuno-suppressive Activity and TITLE OF INVENTION: Toxicity of Monoclonal Antibodies NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                                                                                                                                                                                                                                                 Phillip M. TRANSFERRIN RECEPTOR SPECIFIC TRANSFERRIN RECEPTOR ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT CONJUGATES
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                                                               Sequence 44, Application US/08232246A

Sequence 44, Application US/08232246A

Patent No. 6329508

GENERAL INFORMATION:
APPLICANT. Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DI.
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:
ADDRESSE: How Militia Drive
CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,246A
FILING DATE: US/08/232,246A
FILING DATE: US/08/232,246A
FILING DATE: US/08/232,246A
FILING DATE: US/08/232,246A
FILING DATE: US/08/232,246A
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FILING DATE: US/08/232,246A
FILING DATE: US/08/232,246A
FILING DATE: US/08/232,246A
FILING DATE: US/08/232,246A
FILING DATE: US/28/232,246A
FILING DATE: US/28/2322,246A
FILING DATE: US/28/2322
FILING DATE: US/28/2322
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FILING DATE: US/28/232
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FILING DATE: US/28/23
FILING DATE: US/28/23
FILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02173
COMPUTER READABLE FORM:
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Sequence 4, Application US/08557050
Patent No. 6491916
GENERAL INFORMATION:
APPLICANT: Bluestone, Jeffrey A.
APPLICANT: Zivin, Robert A.
APPLICANT: Joilife, Linda K.
TITLE OF INVENTION: THE IMMON-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, white & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IER COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
93.5%; Score 549; DB 2;
Best Local Similarity 94.5%; Pred. No. 1.8e-57;
Matches 103; Conservative 2; Mismatches 4
                                                  ZIP: 77210 c
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,116A
FILING DATE: 01-JUN-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:082
TELECOMMUNICATION INPORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids

"TELEFAX: amino acids
"TELEFAX: amino acids
                             United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.O. Box 4433
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MOLECULE TYPE: protein
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STATE: Texas
COUNTRY: Unit
ZIP: 77210
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US-08-557-050-4
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δ g RESULT 5 US-08-070-116A-4 ; Sequence 4, Application US/08070116A ; Patent No. 5885573

GENERAL INFORMATION:
APPLICANT: Zivin, Robert A.
APPLICANT: Jolliffe, Linda

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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US-08-232-246A-30
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Patent No. 6015555
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: ANTI-BODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.5%; Score 549; DB 4; Best Local Similarity 94.5%; Pred. No. 1.8e-57; Matches 103; Conservative 2; Mismatches 4.
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/557,050
FILING DATE: Concurrently Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06198
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/070,116
FILING DATE: 01-JUN-1993
ATTORNEY-AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: 37,259
REFERENCE/DOCKET NUMBER: 37,269
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAM: (512) 414-7577
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-557-050-4
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USA
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COUNTRY: US
ZIP: 02173
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1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFERRIN RECEPTOR SPECIFIC
ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 92.6%; Score 543.5; DB 3; Length 109; Best Local Similarity 92.7%; Pred. No. 8.3e-57; Matches 102; Conservative 5; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC Compatible
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION NUMBER: US/08/232,246A
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTONENEY/AGENT INFORMATION:
AMADE: ACCOUNT OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
FILING DATE: 07-SEP-1989
ATTORNEY AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAZ
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TYPE: amino acid
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REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/08232246A
Patent No. 6329508
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERIN RE
TITLE OF INVENTION: CONJUGATES
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                                                                                                                                                                                          Score 543.5; DB 3; Length 109;
Pred. No. 8.3e-57;
5; Mismatches 2; Indels 1
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC COMPALIALE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,539D
FLING DATE: 21-Apr-1994
CLASSIFICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/178583
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 92.2%; Score 541; DB 2; Best Local Similarity 97.1%; Pred. No. 1.6e-56; Matches 101; Conservative 1; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: IGE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 60, Application US/08232539D Patent No. 5965709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: POT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 30.
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
PRAGMENT TYPE: internal
                                                                                                                                                                                              92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1 DNA way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino Acid
                                                                                                                                                                                          Query Match
Best Local Similarity 92.77
Matches 102; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      US-08-232-246A-30
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US-08-232-539D-60
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1 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 60
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                                                                                                                                                                                                                                                                                                                                                    OR DIAGNOSTIC AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                       67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                    61 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                     Sequence 38, Application US/0844644

Patent No. 6015555

GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
APPLICANT: TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 415AAAZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION 1973

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-ULL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wagner, Richard W. REGISTRATION NUMBER: 34,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 110 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two.
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CLASSIFICATION:
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                                                                                                                                                                                       RESULT 10
US-08-444-644-38
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Indels

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     Sequence 18, Application US/08232246A

Partent No. 6328508

GENERAL INFORMATION:
APPLIANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: AOUNGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Lexington
STREET: Lexington
STREET: Lexington
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                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATPONENTY/AGENT INFORMATION:
AMADER: US-SEP-1989
ATTONENTY/AGENT INFORMATION:
AMADER: US-SEP-1989
ATTONENTY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 110 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                 USA
US-08-232-246A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-232-246A-38
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
ZIP: 0217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-569-147-85
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Sequence 85, Application US/08569147
Patent No. 6180377
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANISED ANTIBODIES

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1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SELLGGESVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/09281760E
; Sequence 36, Application US/09281760E
; Retent No. 6734287
; GENERAL INFORMATION:
APPLICANT: Lawton, Robert
; APPLICANT: Mermer: Brion
TITLE OF INVENTION: Specific Binding Protein for Treating
TITLE OF INVENTION: Specific Binding Protein for Treating
TITLE OF INVENTION: Canine Allergy
FILE REFERENCE: 01-1275A
CURRENT FILING DATE: 1999-03-30
FRIOR APPLICATION NUMBER: US/09/281,760E
CURRENT FILING DATE: 1998-04-09
NUMBER: OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
LENGTH: 107
                                                                                                                                                STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: US/08/569,147
APPLICATION NUMBER: US/08/569,147
FILING DATE: 25-March-1996
CLASSIFICATION: 536
ATTORNSY AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REFERENCE/DOCKET NUMBER: CARP-0047
TELECOMMULATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 344; DB 3; Length 66;
Pred. No. 2e-33;
1; Mismatches 2; Indels
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Oo 6180377ris, LLP STREET: One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (136)..(136)
LOCATION: (136)... stands for any nucleic acid
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.6%;
Best Local Similarity 95.5%;
Matches 63; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-569-147-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PREEQY 66
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US-09-281-760E-36
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7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 GVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
28.4%; Score 166.5; DB 2; Length
Best Local Similarity 34.3%; Pred. No. 4.4e-12;
Matches 35; Conservative 22; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 NGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTK 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 152; DB 3;
Pred. No. 2.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFRENCE: P0718PZCIDI
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1992-01-06
PRIOR APPLICATION NUMBER: US 07/794,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Mismatches
                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
                                                                                                                                                                                                                                                                                                                                           P0718P3
                                                                       FILING DATE: 21-Apr. 1994
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 07-JAN 1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SVOBOGA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 99,044
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 65/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
         WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 106 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-08-466-163B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-232-539D-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-466-163B-1
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29.8%; Score 175; DB 4; Length 107;
Best Local Similarity 35.0%; Pred. No. 4.3e-13;
Matches 36; Conservative 23; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (530)...(530)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
LOCATION: (413)..(414)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                    NAME/KEY: misc feature
LOCATION: (451)..(451)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (460)..(462)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                        LOCATION: (500)..(500)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (847)..(849)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (853)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (1382)..(1382)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (1832)..(1832)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 54, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: 19E Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                             NAME/KEY: misc feature LOCATION: (500)..(500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (853)..(853)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DNA Way
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65 NGTLTVTSTLPVGTRDWIEG-ETQCRVTHPHLPRALMRSTTK 105

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Search completed: November 17, 2005, 07:53:56 Job time : 24.6073 secs Sequence Sequence Sequence

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4, At 294,

Sequence Seq

score:

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Sequence:

OM protein -

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Run

Scoring table:

Total number

Database

Searched:

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Sequence 9, Application US/10359318
| Sequence 9, Application US/10359318
| Publication No. US20050215768A1
| GENERAL INFORMATION:
| APPLICANT: Armour, Kathryn L
| APPLICANT: Clark, Michael R
| TITLE OF INVENTION: Polypeptides including modified constant regions
| FILE REFERENCE: 39-302
| CURRENT APPLICATION NUMBER: US/10/959,318
| CURRENT APPLICATION NUMBER: POT/GB2004/004254
| PRIOR APPLICATION NUMBER: POT/GB2004/004254
| PRIOR APPLICATION NUMBER: GB0324368.0
| RIOR APPLICATION NUMBER: GB0324368.0
| RIOR FILING DATE: 2003-10-17
| NUMBER OF SEQ ID NOS: 27
| SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPVAGGBSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Variant of Human 1gG1 CH2 sequence with delta a, OTHER INFORMATION: mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
US-10-370-749-23

US-10-959-318-1

US-110-0259-318-1

US-10-207-655-220

US-10-959-318-21

US-10-959-318-21

US-11-018-102-24

US-10-959-318-21

US-10-359-318-22

US-10-359-318-22

US-10-359-318-25

US-10-959-318-15

US-10-959-318-15

US-10-959-318-15

US-10-959-318-15

US-10-959-318-23

US-10-959-318-23

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US-10-959-318-24

US-10-959-318-24

US-10-959-318-24

US-10-959-318-17

US-10-959-318-17

US-10-959-318-17

US-10-959-318-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 579; DB 18;
Pred. No. 1.1e-48;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 18 Similarity 99.1%; 109; Conservative (
   LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-959-318-9
                                                                                                                                                                                                      548.5
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Best Local S
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Matches
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                                                                              ; Search time 83.1279 Seconds (without alignments) 553.666 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Ag
Sequence 8, Ag
Sequence 11, Ag
Sequence 23, Ag
Sequence 23, Ag
Sequence 25, Ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                     APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK
                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*

1: \cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: \cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*
3: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
6: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
7: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
9: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
11: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
12: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
14: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
15: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
16: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
17: \cgn2_6/ptodata/1/pubpaa/USO10_PUBCOMB.pep:*
18: \cgn2_6/ptodata/1/pubpaa/USO10_PUBCOMB.pep:*
19: \cgn2_6/ptodata/1/pubpaa/USO10_PUBCOMB.pep:*
19: \cgn2_6/ptodata/1/pubpaa/USO10_NEW_PUB.pep:*
21: \cgn2_6/ptodata/1/pubpaa/USO10_NEW_PUB.pep:*
22: \cgn2_6/ptodata/1/pubpaa/USO10_NEW_PUB.pep:*
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FEATURE:
OTHER INFORMATION: Variant of Human 1gG1 CH2 sequence with delta a and d (Q268)
OTHER INFORMATION: mutations
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) FEATURE:
) OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and e (E268)
) OTHER INFORMATION: mutations
US-10-959-318-14
                                                                   1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK 60
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Publication No. US20050215768A1

GENERAL INFORMATION:

APPLICANT: Armour. Kathryn L

APPLICANT: Clark, Michael R

TITLE OF INVENTION: Polypeptides including modified constant regions

FILE REFERENCE: 39:302

CURRENT APPLICATION NUMBER: US/10/959,318

CURRENT FILING DATE: 2004-10-07

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-17

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 14

SEQ ID NO 14
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Sequence 7, Application US/10959318

Publication No. US2005021768A1

GENERAL INFORMATION:

APPLICANT: Armour. Kathryn L

APPLICANT: Clark, Michael R

TITLE OF INVENTION: Polypeptides including modified constant regions

FILE REFERENCE: 39-302

CURRENT APPLICATION NUMBER: US/10/959,318

CURRENT FILING DATE: 2004-10-07

PRIOR PILING DATE: 2004-10-07

PRIOR PILING DATE: 2003-10-17

RIOR APPLICATION NUMBER: GB0324368.0

PRIOR PILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Version 3.3

SEQUENCE: Application Version 3.3
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Pred. No. 2.4e-47;
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96.4%;
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-959-318-14
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Publication No. US20050215768A1

GENERAL INFORMATION:

APPLICANT: Armour, Kathryn L

APPLICANT: Armour, Michael R

TITLE OF INVENTION: Polypeptides including modified constant regions

FILE REPERENCE: 2004-10-07

CURRENT APPLICATION NUMBER: DCT/GB2004/004254

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-17

PRIOR FILING DATE: 2003-10-17

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.3

SEQ ID NO 13

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Sequence 10, Application US/10959318

Publication No. US20050215768A1

GENERAL INFORMATION:
APPLICANT: Armour, Kathryn L

APPLICANT: Clark, Michael R

TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302
CURRENT FILING DATE: 2004-10-07

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 10

LENGTH: 110
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Pred. No. 2.4e-47;
1; Mismatches 3; Indels
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98.6%; Score 579; DB 18;
Best Local Similarity 99.1%; Pred. No. 1.1e-48;
Matches 109; Conservative 0; Mismatches 1;
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Best Local Similarity 96.4%;
Matches 106; Conservative
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Publication No. US20050215768A1

Publication No. US20050215768A1

GENERAL INFORMATION:

APPLICANT: Armour, Kathryn L

APPLICANT: Clark, Michael R

TITLE OF INVENTION: POLYDeptides including modified constant regions

FILE REFERENCE: 39-302

CURRENT APPLICATION NUMBER: US/10/959,318

CURRENT APPLICATION NUMBER: PCT/GB2004/004254

PRIOR APPLICATION NUMBER: PCT/GB2004/004254

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.3

SEQ ID NO 8

LENGTH: 110
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Publication No. US200502157681

GENERAL INFORMATION:
APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: POlypeptides including modified constant regions
TITLE OF INVENTION: POlypeptides including modified constant regions
FILE REPERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT PILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: PG7/GB2004/004254
PRIOR PILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: GB0324368.0
PRIOR FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE PARENTIN VERSION 3.3
SEQ ID NO 11
LENGTH: 109
                                                                                                                                   1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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                                           Length 110;
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95.9%; Score 563; DB 18; Length 110;
Best Local Similarity 96.4%; Pred. No. 3.8e-47;
Matches 106; Conservative 1; Mismatches 3; Indels
                                                                                          Indels
                                             Score 563; DB 18;
Pred. No. 3.8e-47;
                                                                                          1; Mismatches
                                             95.9%;
96.4%;
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                                        Query Match
Best Local Similarity 96.14
Matches 106; Conservative
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US-10-959-318-8
US-10-959-318-7
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and d (D268)
; OTHER INFORMATION: mutations
US-10-959-318-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e (E268)
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Publication No. US20050136061A1
GENERAL INFORMATION:
APPLICANT: Centocor.
1TTLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
FILE REPERENCE: CEN5045 USA NP
CURRENT APPLICATION NUMBER: US/11/018,102
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
CTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, b and
CTHER INFORMATION: mutations
US-10-959-318-12
                                                                                                                                                                                                                                                                                                            1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-10-959-318-12
| Sequence 1.2 Application US/10959318
| Publication No US2005021576841
| GENERAL INFORMATION:
| APPLICANT: Armour, Kathryn L
| APPLICANT: Clark, Michael R
| TITE OF INVENTION: Polypeptides including modified constant regions
| FILE REFERENCE: 39-302
| CURRENT FILING DATE: 2004-10-07
| PRIOR ALLING DATE: 2004-10-07
| PRIOR FILING DATE: 2003-10-17
| NUMBER OF SEQ ID NOS: 27
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: PatentIn version 3.3
| SEQ ID NO 12
                                                                                                                                                                                                                                                                                  1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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Pred. No. 4.2e-47;
0; Mismatches 1; Indels 1;
                                                                                                                                                                               Score 562.5; DB 18; Length
Pred. No. 4.2e-47;
0; Mismatches 1; Indels
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Best Local Similarity 98.2%;
Matches 108; Conservative
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ORGANISM: Artificial Sequence
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SEQ ID NO 23
LENGTH: 110
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Best Local Similarity 98.2<sup>3</sup>
Matches 108; Conservative
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US-11-018-102-25
US-11-018-102-25
Sequence 25, Application US/11018102
Publication No. US20050136061A1
GENERAL INFORMATION:
APPLICANT: Centcoor, Inc.
TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
FILE REFREENCE: CENSO45 USA NP
CURRENT APPLICATION NUMBER: US/11/018,102
CURRENT FILING DATE: 2004-12-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.3
SEQ ID NO 25
LENGTH: 110
                                                                                                                                                                                                                           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Sequence 270, Application US/10627556;
Publication No. US20050136049A1
GENERAL INFORMATION:
APPLICANT: LEDBETTER, ARTHA
APPLICANT: THOMPSON, PETER A.
TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF;
FILE REFERENCE: 49076.000044.CIP2
CURRENT APPLICATION NUMBER: US/10/627,556
CURRENT APPLICATION NUMBER: US/10/63,530
PRIOR FILING DATE: 2002-01-17
PRIOR PELING DATE: 2002-01-17
PRIOR PELING DATE: 2002-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/765,208
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2002-06-03
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95.2%; Score 559; DB 20;
Best Local Similarity 95.5%; Pred. No. 9.4e-47;
Matches 105; Conservative 2; Mismatches 3;
                    ; FEATURE:
; OTHER INFORMATION: engineered G1 CH2
US-11-018-102-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: engineered G4 CH2 US-11-018-102-25
ORGANISM: Artificial
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; Publication No. US20050215768A1
; Publication No. US20050215768A1
; GENERAL INFORMATION:
    APPLICANT: Clark, Michael R
; TITLE OF INVENTION: Polypeptides including modified constant regions
    TITLE OF INVENTION: Polypeptides including modified constant regions
    FILE REFERENCE: 39-302
    CURRENT APPLICATION NUMBER: US/10/959,318
    CURRENT PILING DATE: 2004-10-07
    PRIOR PILING DATE: 2004-10-07
    PRIOR PILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                   2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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                                                                                                                            FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: amino acid sequence
US-10-627-556-270
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Pred. No. 1.2e-46;
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US-10-370-749-23
US-10-370-749-23
Sequence 23, Application US/10370749
Publication No. US20040002587A1
GENERAL INFORMATION:
APPLICANT: Warkins, Jeffry D.
APPLICANT: Allan, Barrett
TITLE OF INVENTION: FC Region Variants
TITLE PREFERENCE: AME-07823
CURRENT APPLICATION NUMBER: US/10/370,749
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/358,161
PRIOR APPLICATION DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Version 3.2
SEQ ID NO 23
                                                                                                                                                                                                                                                            Query Match
95.1%; Score 558; DB
Best Local Similarity 95.4%; Pred. No. 1.2e
Matches 104; Conservative 2; Mismatches
SOFTWARE: PatentIn version 3.2
SEQ ID NO 270
LENGTH: 109
                                                                              TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 94.5
Matches 104; Conservative
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Publication No. US20050136061A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
FILE REFRENCE: CEN5045 USA NP
CURRENT APPLICATION NUMBER: US/11/018,102
CURRENT FILING DATE: 2004-12-21
NUMBER OF SEQ ID NOS: 28
SOTUWARE: Patentin version 3.3
SEQ ID NO 2.2
SEQ ID NO 2.2
TYPE: PRT
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Sequence 220, Application US/10207655

Publication No. US20030118592A1

GENERAL INFORMATION:

APPLICANT: Ledbetter, Jeffrey A.

APPLICANT: Hayden-Ledbetter, Martha S.

TITLE OF INVENTION: BIDING DOMAIN-IMMUNGLOBULIN FUSION PROTEINS

FILE REFRENCE: 390069.401C1

CURRENT APPLICATION NUMBER: US/10/207,655

CURRENT APPLICATION NUMBER: US/10/207,655

CURRENT PILING DATE: 2002-07-25

NUMBER OF SEQ ID NOS: 426

SOFTWARE: Patentin version 3.0

SEQ ID NO 220
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94.9%; Score 557; DB 20; Length 110;
Best Local Similarity 94.5%; Pred. No. 1.5e-46;
Matches 104; Conservative 2; Mismatches 4; Indels (
                                                                                                                                                                                             4; Indels
                                                                                                                                              Query Match

94.9%; Score 557; DB 18;
Best Local Similarity 94.5%; Pred. No. 1.5e-46;
Matches 104; Conservative 2; Mismatches 4;
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SOFTWARE: Patentin version 3.3 SEQ ID NO 1
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ORGANISM: Artificial Sequence
                                   LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
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US-11-018-102-22
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US-11-018-102-22
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94.2%; Score 553; DB 14; Length 109;

Query Match

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WPI; 2003-616080/58.
N-PSDB; ADM33854.
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Human GCS
                                                                                                                            November 17, 2005, 06:38:35; Search time 91.6667 Seconds (without alignments) 464.112 Million cell updates/sec
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Aae32630 B
Aao30892 B
                                                                                                                                                                                                                                                                                                                                                                                                                                             2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                        2105692 seqs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*

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Maximum DB
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Human IgG	Anti-inte	Amino aci	Human IgG	Human	Human 1gG	Anti-tiss	IL4.Y124D	IL4.Y124D	Leptin 1-	Leptin 1-	Heterolog	Human IFN	Interfero	Humanised	Human 1gG	Amino aci	Protein 8	Humanized
Ade97357	Adm41543	Aaw70801	Aay92190	Abw02169	Ad135097	Abr42735	Aar90922	Aar90921	Aaw10534	Aaw10535	Add32018	Aay17903	Aaw18579	Aaw13564	Aay31672	Abr55342	Adc73234	Adf69629
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ADE97357	ADM41543	AAW70801	AAY92190	ABW02169	ADL35097	ABR42735	AAR90922	AAR90921	AAW10534	AAW10535	ADD32018	AAY17903	AAW18579	AAW13564	AAY31672	ABR55342	ADC73234	ADF69629
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327	327	329	329	329	329	330	382	382	396	396	403	432	433	443	444	444	444	444
96.9	96.9	6.96	6.96	96.9	6.96	6.96	6.96	6.96	6.96	6.96	6.96	6.96	6.96	6.96	6.96	6.96	6.96	6.96
565 7	565	565	565	565	565	565	565	265	565	565	265	265	565	565	565	565	565	565
9.5	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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ADM33855

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Britan HuBPO-L-VFcgamma4 fusion protein.

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Expthropoietin; EPO; immunoglobulin; IgG;

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Fragment crystallisation regions, Fc; chronic anaemia; renal disease;

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MAC-Odyplastic syndrome; (HuEPO)-L-VFcgamma4; human.

COS

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Monce "signal peptide"

FFT Protein (note "wild-type Ser substituted by Pro"

FFT Protein (note "wild-type Leu substituted by Ala"

Misc-difference 219

FFT Misc-difference 219

FFT Misc-difference 219

FFT Misc-difference 219

COCE "wild-type Leu substituted by Ala"

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CSUNL): SUN L K.

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fusion protein comprising HibbO, a peptide linker, and a human comprising the function region) variant. Also immunoglobulin GFC (fragment crystallisation region) variant. Also included is a carbohydrate-derived cell line producing the human carybropoietin-L-VFC fusion protein cited above in its growth medium in expense of 10 microgramme per million cells in a 24-hour period. The HubbO cevess of 10 microgramme per million cells in a 24-hour period. The HubbO cere in vitro biological activity of at least 2-fold relative to that of recombinant HubbO on a molar basis. The flaxible peptide linker containing about 20 or fewer amino acid mutations to attenuate effector functions. The human igg Fc contains amino acid mutations to attenuate effector functions. The human iggs with human igg with Ser228Pro and Leu235Ala mutations. The Proj31Ser mutation, human igg4 with Ser228Pro and Leu235Ala mutations or cerembinant human erythropoietin-L-VFC fusion protein are useful for treating patients with chronic anaemia caused by renal failure, cancer chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV consolution, or myelodysplastic syndrome. The increased activity and protein in the serum, as compared to prior art, leads to lower dosages and less frequent injections means improved safety and tole-aballity, and less frequent injections means improved safety and tole-aballity, and less frequent injections result in better patient compliance and quality of life. The present sequence represents the fusion protein HUEPO-L-VFCgamma4. invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc recombinant human erythropoietin-L-vFc fusion proteins, useful for treating patients with chronic anemia caused by renal failure, cancer chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV Claim 4; Fig 2B; 14pp; English. infection

Sequence 437 AA;

1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60 0; Gaps 61 PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 97.8%; Score 570; DB 7; Length 437; 98.2%; Pred. No. 7.9e-49; ive 0; Mismatches 2; Indels Matches 108; Conservative Query Match Best Local Similarity g ò

ADR48986 standard; protein; 437 AA HuBPO-L-vFc fusion protein #1. ADR48986;

02-DEC-2004 (first entry)

antianaemic; nephrotropic; human; HuBPO-L-vFc; erythropoietin; EPO; anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis; AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.

Homo sapiens. Synthetic. US2004175824-A1

09-SEP-2004.

21-JAN-2004; 2004US-00761593

17-AUG-2001; 2001US-00932812

SUN L K.
SUN B N C.
SUN C R Y. (SUNE/) (SUNC/) Sun CRY; Sun BNC, Sun LK,

WPI; 2004-634851/61. N-PSDB; ADR48985. New recombinant HuBPO-L-vFc fusion protein comprises human erythropoietin (HuEPO), a peptide linker, and a human IgG Fc variant, useful for treating chronic anemia due to renal diseases, cancer chemotherapy, or rheumatoid arthritis.

Claim 4; SEQ ID NO 20; 31pp; English.

The Recombinant Husevi-Lavyer (Handon protein comprises numan eryturoposetin to the Tecombinant Husevi-Lavyer than a human 1gG Fe variant, is new.

CHUBERNONE CLAIME are also included for the following: a chinese hameter ovary (CHO)-derived cell line producing the Huspo-LavFe fusion protein in the great of the making a recombinant that on the comprising period; and a method for making a recombinant that on order 1s present berein an enth of the making a recombinant that on order 1s present berein. The human 1gG Fe variant comprises a hinge, CH2, and CH3 domains of human 1gG Avariant comprises a hinge, CH2, and CH3 domains of human 1gG Fe variant comprises a hinge, CH2, and CH3 domains of human 1gG Fe variant comprises a hinge, CH2, and CH3 domains of human 1gG With Pro31315es mutations comprising 437 amino acids (SEQ ID NO. 18). It also comprises a hinge, CH2, and CH3 domains of human 1gG with Leu234041, Leu234041, Leu234041, and Pro31315er mutations comprising 437 amino acids (SEQ ID NO. 20). It further comprises a hinge, CH2, and CH3 domains of human 1gG with Leu234041, Leu234041, and Pro31315er mutations comprising 437 amino acids (SEQ ID NO. 20). It further comprises a hinge, CH2, and CH3 domains of human 1gG with Leu234041, and Pro31315er mutations comprising 437 amino acids (SEQ ID NO. 20). It further comprises a hinge, CH2, and CH3 domains of human 1gG Fe contains amino acid mutations to attended the human 1gG Fe contains amino acid mutations to attended the human 1gG Fe contains amino acid mutations to attended the human 1gG Fe contains amino acid mutations to attended the human 1gG Fe contains and a molar basis. Preferred Method Making a recombinant the Law 1900 protein exhibites in vitro obiological activity similar to or higher than the 1gG Fe contains amino acid mutations to attended cell line where the recombinant protein is expressed in exhibite in vitro biological activity similar to or higher than the respect of the off similar protein receins exhibite an vitra part protein or mutation part and and incorporates a BamHI site. The resulting DNA fragments of approximately 600 bp were inserted into a holding vector such as pUC19 at the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the human EPO gene was confirmed by DNA sequencing. For the convenience of cloning, SEQ ID NO. 1 which incorporates a restriction enzyme cleavage site is used as the 5' oligonucleotide primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin

Sequence 437 AA;

Gaps Score 570; DB 8; Length 437; Pred. No. 7.9e-49; 0; Mismatches 2; Indels 0; 97.8%; 98.2%; Query Match
Best Local Similarity 98.2
Matches 108; Conservative

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sequence of human GCSF-L-fragment of crystallisation gamma 4 variant

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Gaps

; 0

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Pred. No. 8.2e 0; Mismatches Score 570;

Conservative

Query Match Best Local Similarity Matches 108; Conser

Sequence 449 AA; fusion protein.

Length 449 Indele

7; 8.2e-49

DB

97.8%; 98.28; 9

APEFAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 292

233 61 293

PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110

1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-
Vef fusion protein for treating immune or hematopoietic system disorders
comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin (
Fc variant.
          APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                          Human GCSF-L-fragment of crystallisation gamma 4 fusion protein.
                                                    PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                               PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 330
                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild type Leu substituted by Ala"
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                                                                                                                          ADM33378 standard; protein; 449
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                                                                                                                                                                                                                                                                                         sapiens
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                                                                                                                                                 ADM33378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibodies binding to porcine but not human cell interaction proteins useful to treat and assay for rejection of xenografted porcine organs, tissues or cells.
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PREEGENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 342
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                                                                                                                                                                                                            Xenotransplantation, graft rejection, cell interaction, pig; vascular cell adhesion molecule, VCAM; monoclonal antibody;
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Pred. No. 1.9e-48;
0; Mismatches 0;
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                                                                                                                                                                                   2A2 (Chimeric) human G2/G4 chimeric antibody.
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                                                                                 AAW14933 standard; protein; 462
                                                                                                                                                                                                                                           chimeric antibody; diagnosis.
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99.1%;
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96US-00004489
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                                                                                                                                           (revised)
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N-PSDB; AAT62931.
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Matches 109; Conserv
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                                                                                                                                                                                                                                                                        Homo; sapiens
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26-SEP-1996;
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16-JUN-1997
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The invention describes a recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-vFc fusion protein comprising hG-CSF, a peptide linker, and a human immunoglobulin G (IgG) Fc variant. Also described are: a CHO-derived cell line producing the above hG-CSF-L-vFc fusion protein in its growth medium in excess of 10 kmgr;g per million cited above, comprising generating a CHO-derived cell line cited above, growing the cell line under conditions the recombinant fusion protein is expressed in its growth medium, and purifying the expressed protein. The recombinant fusion protein is useful in treating a variety of conditions associated with an impaired immune or haematopoietic system, including cancer chemotherapy, leukkemias, anaemias, AlDS, bone marrow transplantation, and chronic neutropenias. This is the amino acid

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RESULT 6
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                  247 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 305
 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                  Matis LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibodies binding to porcine but not human cell interaction proteins useful to treat and assay for rejection of xenografted porcine organs, tissues or cells.
                                        PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                            PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 355
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                                                                                                                                                                                                             Xenotransplantation, graft rejection, cell interaction, pig
vascular cell adhesion molecule, VCAM, monoclonal antibody,
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Pred. No. 1.9e-48;
0; Mismatches 0;
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                                                                                                                                                                                         2A2 (Chimeric) human G2/G4 chimeric antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Mueller EE,
                                                                                                                AAW14934 standard; protein; 462 AA
                                                                                                                                                                                                                                   chimeric antibody; diagnosis.
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99.1%;
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96US-00004489
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Best Local Similarity 99.1'
Matches 109; Conservative
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N-PSDB; AAT62932.
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16-JUN-1997
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247 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 305

306 PREEQFNSTYRVVSVLTYLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 355

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61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110

1 APPVAGGPSVFLFFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK

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Gaps

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A chimeric antibody (AAW14939) comprises the C1 and hinge regions of human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal antibody (MAb) 3F4 heavy chain variable region sequence (see also AAW14938). The chimeric antibody is specific for porcine VCAM It is useful for diagnosing human rejection of porcine exentransplants and for improving xenotransplants and for human recipients. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                       Xenotransplantation; graft rejection; cell interaction; pig; vascular cell adhesion molecule; VCAM; monoclonal antibody; chimeric antibody; diagnosis.
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99.1%; Pred. No. 1.9e-48;
ive 0; Mismatches 0;
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                                                                                                                                                                        3F4 (Chimeric) human G2/G4 chimeric antibody.
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AAW14939 standard; protein; 463 AA.
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Matches 109; Conservative
                                                                                                  (revised)
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N-PSDB; AAT62936.
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26-SEP-1996;
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16-JUN-1997
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                                                                           Xenotransplantation; graft rejection; cell interaction; pivascular cell adhesion molecule; VCAM; monoclonal antibody
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Pred. No. 1.9e-48;
0; Mismatches 0
                                             3F4 (Chimeric) human G2/G4 chimeric antibody.
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                                                                                                          chimeric antibody, diagnosis.
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96US-00004489.
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   (revised)
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                                                                                                                                         Homo; sapiens
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17-OCT-2003
16-JUN-1997
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                                                                                                                                                                                                                                   03-APR-1997.
                                                                                                                                                                      Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP51695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
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                                                                                                                                                           Мив вр.
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A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.

Renshaw M;

Barbas-Frederickson S,

Bowdish KS,

WPI; 2002-566610/60 N-PSDB; ABQ73374

05-DEC-2000; 2000US-0251448P. 04-MAY-2001; 2001US-028889P. 29-MAY-2001; 2001US-0294068P.

(ALEX-) ALEXION PHARM INC.

05-DEC-2001; 2001WO-US047656.

WO200246238-A2

13-JUN-2002

Homo sapiens.

Synthetic.

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The present into present the complementary determining region (CDR) are reglaced or fused with biologically active perfides e.g. a peptide minetic such as an erythropoietin (TEPO) or thrombopoietin (TPD) minetic, that is flanked with proline at its carboxy terminus. (I) has minetic such as an erythropoietin (EPO) or thrombopoietin (TPD) minetic, that is flanked with proline at its carboxy terminus. (I) has minetic, antianemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful corresponding proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, which results in increased platelet promegakaryocytes or megakaryocytes, which results in increased platelet promegakaryocytes or megakaryocytes, which results in increased platelet correct of the CDRs is replaced with a EPO minetic, or which has one or more of its CDRs fused to an EPO minetic, is useful for increasing the production of red blood cells, where (I) is contacted with has one or the appearance of the blood cells, where (I) is one contacted with has mentopoietic stem cells or their progenitors. (I) is useful for diagnostics or therapeutics, in cell isolation strategies, and for treating patients are suffering from deficiency in cell populations caused by disease.

ABO73288 to ABO73377 and ABP51669 to ABP51696 represent sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an immunoglobin molecule or its fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREEQFISTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.2%; Score 566.5; DB 5; Length 472; 99.1%; Pred. No. 2e-48; ive 0; Mismatches 0; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 13A; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ16647 standard; protein; 472 AA.
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tes 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-SEP-2004
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92WO-US010206 91US-00800458

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WO9310819-A1.
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                                                                                                                        26-NOV-1991;
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                                                                      10-JUN-1993
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                                                                                                                                                                               Friden PM:
                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                        comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRS) are replaced with a peptide mimetic selected from an erythropoietin (BPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents an immunoglobulin antibody heavy chain of
                          immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive; immunotherapy; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with EPO mimetic or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymerase chain reaction, primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaccutical; gamma-3; gamma-4; diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel immunoglobulin molecule or its fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.2%; Score 566.5; DB 8; Length 472; 99.1%; Pred. No. 2e-48;
Immunoglobulin antibody 5G1.1-TPO heavy chain SEQ ID NO:67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Undefined ORF2 encoded by plasmid pAH4808.
                                                                                                                                                                                                                                              Renshaw M;
                                                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO 67; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR41717 standard; protein; 110 AA.
                                                                                                                                                              17-NOV-2003; 2003WO-US036894
                                                                                                                                                                                                                                            Bowdish KS, Frederickson S,
                                                                                                                                                                                        02-DEC-2002; 2002US-00307724
                                                                                                                                                                                                                  (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Matches 109, Conservative
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                                                                                                                                                                                                                                                                       WPI; 2004-460973/43
                                                                                                                                                                                                                                                                                 N-PSDB; ADQ16648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 472 AA;
                                                                                                         WO2004050017-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
                                                                                                                                     17-JUN-2004
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20-OCT-1993
                                                                               Synthetic
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ID AAR
XX AC AAR
XX AC AAR
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The sequences given in AAR41715-18 are encoded by the expression vector pAH4808. This vector represents the cloning of the human gamma isotype, gamma-4, with the variable region of the murine monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences corocity of the combination with the chimeric light chain vector, pAG4611 (see also AQ43845), was transfected into SP2/0 cells and clones were isolated. In combination with the chimeric light chain vector, pAG4611 (see also AQ43845), was transfected into SP2/0 cells and clones were isolated. This an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APERLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                            Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of native IgG Fc region humIgG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.9%; Score 565; DB 2; L6 97.3%; Pred. No. 4.9e-49; ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 19J; 151pp; English.
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Best Local Similarity 97.3
Matches 107; Conservative
(ALKE-) ALKERMES INC
                                                                                                                                                                         WPI; 1993-196742/24.
                                                                                                                                                                                                            N-PSDB; AAQ43848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 110 AA;
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New

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This invention relates to non-naturally occurring peptide ligands which bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides crepresented in AAB76320 - AAB76421 - AAB76509 are examples of the ErbB2 binding ligands of the invention. Sequences AAB76421 - AAB76431 represent antibody Fc amino acid sequences used in the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers, diseases of the nervous system, musculature and epithelia, e.g. nervous system champer resulting from trauma, surgery, strokes, ischaemia, infection, metabolic disorders, nutritional deficiency or toxic agents. In Eccion, particular the synthetic peptide ligands may be used to treat Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy associated with diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APEFLGGPSVFLFPPKPKDILMISKTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61
                                                                                                            Non-naturally occurring peptide ligands which compete for binding human erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel fusion polypeptides comprising a peptide ligand domain which functions to target hybrid molecule to target cell, and immunoglobulin constant region multimerization domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusion protein; immunoglobulin; multidimerization domain; ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 565; DB 4;
Pred. No. 1.1e-48;
0; Mismatches 3;
                                                                                                                                                                                                             Disclosure; Fig 2A; 116pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                  WPI; 2001-123048/13.
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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 218 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IgG4
                      Dennis MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                         AAB07474-78 represent native IgG Fc regions. The proteins are used to produce Fc region-containing polypeptides that have altered effector function as a consequence of one or more amino acid modifications in the Fc region. The variant polypeptides are useful for treating cancer, allergic conditions such as asthma (with an anti-lgE antibody), and LFA-1-mediated disorders. Where the polypeptide binds the HER2 receptor, the disorder preferably is HER2-expressing cancer, e.g. a benign or malignant tumour characterized by overexpression of the HER2 receptor. Such cancers include breast cancer, gauamous cell cancer, small-cell lung cancer, gatomous, cancer, panceratic cancer, glioblastoma, cervical cancer, ovarian cancer, bladder cancer, hepatoma, colon canner, colorectell cancer, endometrial cancer, hepatoma, carcinoma, kidney cancer, liver cancer, prostate cancer, wulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck
                                                                                                                                                                                                                                   Fc region-containing polypeptides that have altered effector function to one or more amino acid modifications in the Fc region, useful in treatment of cancer and allergic conditions such as asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve dedifness; Meniere's disease; diabetic neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 565; DB 3;
Pred. No. 1.1e-48;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human 1gG4 Fc region amino acid sequence.
                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 22A; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB76425 standard; protein; 218
14-JAN-2000; 2000WO-US000973.
                                            99US-0116023P.
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Best Local Similarity 97.3%;
Matches 107; Conservative
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                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
                                                                                                                                                                                       WPI; 2000-476035/41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200101748-A2
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                                            15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                        Presta LG;
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Length 218; Indels

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                                            The present invention relates to a fusion protein, comprising a peptide ligand and an immunoglobulin (1g) constant region multimerization domain (1b). The hybrid molecules comprising the peptide ligands and their functional derivatives can be used in the same applications as, a peptide ligand can be used. For example the peptide ligand can bind ErbB2. The peptide ligand may bind to and inhibit the activity associated with a particular target molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to an isolated antibody comprising a dimerisation domain and three or more antigen binding sites amino-terminal to the domain. It is cytostatic, antiinflammatory, antibacterial, immunosuppressive, antiallergic, an apoptosis inducer, a vaccine and used in gene therapy. Along with a cytotoxic agent, is useful for treating a disorder e.g. cancer in a mammal, for inducing apoptosis of a cancer cell, and for killing a B cell or a cell which overexpresses or expresses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel engineered antibody useful in therapeutic applications, contains dimerization domain and three or more antigen binding sites.
                                                                                                                                                                                                                                                                                        APEFLGGPSVFLFPPKFKDTLMISRTPBVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                    1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody dependant cell mediated cytotoxicity; complement dependant cytotoxicity; epidermal growth factor receptor; tumour necrosis factor; lymphocyte; tetravalent antibody, cytostatic; antiinflammatory; antipooriatic; dermatological; antiuloer; antiantentic; antiarteriosclerotic; antirheumatic; antibacterial; antiarthritic; neuroprotective; immunosuppressive; antianaemic;
                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                      Length 218;
                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Native sequence human IgG Fc region sequence humIgG4.
                                                                                                                                                                                                      ; DB 4;
1.le-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiallergic; antidiabetic; gene therapy; human.
                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                      Score 565;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG78436 standard; protein; 218 AA
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                Disclosure; Fig 2; 69pp; English.
                                                                                                                                                                                                 96.98;
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                                                                                                                                                                                                                                    Matches 107; Conservative
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                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                         Sequence 218 AA;
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an ErbB receptor and for treating benign and malignant tumours, inflammatory, angiogenic and immunological disorders, autoimmune diseases, central nervous system inflammatory disorders. The antibody is also useful for immunodiagnosis of various diseases including cancer, for human therapy in redirected cycotoxicity, and also useful as fibrinolytic agents or vaccine adjuvants, useful as affinity purification agent, in diagnostic assays for detecting the expression of antigen of interest in specific cells, tissue or serum, and useful for blocking an immune response to a foreign antigen. The antigen is internalised faster than a bivalent antibody by a cell expressing an antigen to which the antibodies bind. The antibody comprises three or four heavy chain variable domains which are able to combline with three or four havy chain variable domain polypeptides to form three or four antigen binding sites directed against
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                This sequence represents the native sequence human IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the protein sequence of the Fc region of human
1964. A claimed composition comprises a glycoprotein having a Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, antibody, IgG4, cytostatic, immunosuppressive, antiinflammatory, antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising a glycoprotein having a Fc region useful for treating cancer, autoimmune disease, inflammatory disorder or infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A PEFLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APPVAGGPSVFLFPPKPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                                                                                                                 Length 218;
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                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                 Score 565; DB 5;
Pred. No. 1.1e-48;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 23; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR42442 standard; protein; 218
                                                                                                                                                                                                                                                                                                                                                                                    96.98;
97.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-2002; 2002WO-US033739
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                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 107, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human IgG4 Fc region.
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                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                 Fc region, humigG4
                                                                                                                                                                                                                                                                              the same antigen.
                                                                                                                                                                                                                                                                                                                                           Sequence 218 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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About 80-100% of the glycoprotein comprises a mature core carbohydrate structure which lacks fucose attached to the Fc region. The glycoprotein preferably comprises an antibody, and the Fc region is preferably a human 1gG Fc region, especially a human 1gG1, 1gG2, 1gG3 or 1gG4 Fc region. The glycoprotein binds FcgammaRIII with better affinity, or mediates antibody edpendent cell-mediated cytotoxicity more effectively, than the glycoprotein including fucose. The antibody may be chimeric, humanised or human and binds a B-cell surface marker, an ErbB receptor, a tumourassociated antigen or an angiogenic factor, CD20, HRR2, vascular endothelial growth factor, CD40 or prostate stem cell antigen. The composition is useful for treating cancer, autoimmune disease, an inflammatory disorder or infection in a mammal
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Sequence 218 AA;

0; Gaps Query Match 96.9%; Score 565; DB 6; Length 218; Best Local Similarity 97.3%; Pred. No. 1.1e-48; Matches 107; Conservative 0; Mismatches 3; Indels 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60 2 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDFEVQFNWYVDGVEVHNAKTK 61 g

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Search completed: November 17, 2005, 07:04:57 Job time : 93.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

November 17, 2005, 06:49:37; Search time 18.0822 Seconds (without alignments) 585.319 Million cell updates/sec Run on:

US-09-674-857-12 583 Perfect score:

1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
3: pir2:*
5: pir3:*
7: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	gamma-4 chain		gamma chain C	gamma-1	gamma-1 chain	heavy chain V	m	gamma-3 chain	Ig gamma-3 heavy c	gamma 2b	gamma 2a	gamma 4	gamma 3	gamma	heavy chain C		gamma-21	gamma-	heavy ch	gamma-2 chai	gamma-3 chain	gamma-3 chain	gamma-2	Ig gamma-1 chain	gamma-1 chain	onoclonal a	gamma-2c	g gamma-2b	
SUMMARIES	ID	G4HU	G2HU	PT0207	S31866	GHHU	869339	A23511	A60764	G3HUWI	147160	147159	147162	147161	147158	C30554	GHRB	PS0018	S31459	S22080	G2GP	G3MSC	G3MSM	806611	GIMS	GIMSM	PC4436	S00847	G2MSBM	G2MS11
	DB	1	Н	7	4	-	7	7	~	-	7	~	~	~	~	~	Н	~	~	~	Н	Н	Н	~	-	-	7	~	-	П
	Query Match Length	327	326	234	255	330	374	377	377	289	328	328	277	328	328	308	323	333	472	470	329	329	398	327	324	393	4	329		474
d	Query Match	96.9	93.1	ς.		٠	٠	91.1	ä	•	90.6	ö	79.8	•	76.0	74.3	74.3	74.3			73.1				•		69.5	69.1	68.4	68.4
	Score	595	542.5	541	541	541	541	531	531	518	470	470	465	443	443	433	433	433	433	431	426	417	417	409	405	405	405	403	399	399
	Result No.	1	7	m	4	S	9	7	80	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-1 chain C	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma heavy cha	Ig epsilon-chain -	6	Ig gamma-1 chain C	Ig heavy chain pre	Ig epsilon chain C
GZMSAB	G2MSA	G2MSAM	S37483	PS0017	S01321	840295	PS0019	B30503	A30503	146732	136948	ЕННΩ	S14236	S04845	EHRT
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335	330	399	469	326	475	446	322	112	88	180	426	428	152	549	429
67.9	67.4	67.4	67.4	66.7	0.99	65.7	58.8	53.3	47.7	44.3	28.7	28.6	28.3	26.4	25.9
396	393	393	393	389	385	383	343	311	278	258	167.5	166.5	165	154	151
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ALIGNMENTS

RESULT 1

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Gramma-4 chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: 0.2-Apr-1982 #text_change 09-Jul-2004 C;Accession: A90933; A90249; A02150 R;Ellison, J.; Buxbaum, J.; Hood, L. DNA 1, 11-18, 1981 A;Ttle: Nucleotide sequence of a human immunoglobulin C-gamma4 gene. A;Ttle: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
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96.9%; Score 565; DB 1; Length 327;
Best Local Similarity 97.3%; Pred. No. 6.3e-49;
Matches 107; Conservative 0; Mismatches 3; Indels
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111 APPVA-GPSVFLFPPKPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 169
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C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: $31866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Pan troglodytes (chimpanzee)
C.Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                    1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSOEDPEVOFNWYVDGVEVHNAKTK
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;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                              61 PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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          Length 326;
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F;23-255/Region: human 1g gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: PT0207
R; Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A/Title: Nucleotide sequence of chimpanzee Fc and hinge regions. A; Reference number: PT0207; MUID:91287716; PMID:2062315
A; Accession: PT0207
A; Residues: 1-234 CEHR>
C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin homology C; Keywords: immunoglobulin homology < IMM>
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Pred. No. 1.2e-46;
4; Mismatches 5; Indels
                                                                                                                  Indels
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          DB 1;
          Score 542.5; DB 1
Pred. No. 1.1e-46;
3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig gamma-1 chain C region - synthetic
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Query Match
Best Local Similarity 93.6%;
Matches 103; Conservative
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Best Local Similarity 91.8%;
Matches 101; Conservative
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A; Residues: 1-255 <FIL>
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PT0207
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                                                                                       Ig gamma-2 chain C region - human
Cispecies: Homo sapiens (man)
Cipacies: Homo sapiens (man)
Cipacies: 30-Apr.1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
CiAccesion: A93906; A92809; A90752; A93132; A02148
Riblison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
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A;Gene: GDB:1GHG2
A;Gene: GDB:119338; OMIM:147110
A;Gene: GDB:119338; OMIM:147110
A;Gene: GDB:119338; OMIM:147110
A;Gene: GDB:119338; OMIM:147110
A;Gene: GDB:119338; OMIM:147110
A;Gene: GDB:119338; OMIM:147110
A;Gene: GDB:119338; OMIM:147110
A;Gene: GDB:119338; OMIM:147110
A;Gene: GDB:119338; OMIM:147110
A;Gene: GDB:119338; OMIM:147110
C;Gene: GDB:119338; OMIM:147110

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A; Molecule type: protein
A; Residues: 1-19, (0',21-57, 'Z',59, 'A',61-193,'D',195-125 < WAN>
A; Residues: 1-19, (0',21-57, 'Z',59, 'A',61-193,'D',195-125 < WAN>
A; Molec: Tro. 156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains of a A; Reference number: A90752; MUID: 80001357; PMID: 113060
A; Contents: myeloma protein Zie
A; Contents: myeloma protein Zie
A; Molecule type: protein
A; Residues: 1-24, 'E', 26-57, 'EV', 60-85:132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-100, 'C',                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: protein
A,Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-326 <ELL>
A; Residues: 1-326 <ELL>
A; Cross-references: UNIPROT: P01859; GB: V00554; GB: J00230; NID: G32759; PIDN: CAB58438.1;
A; Vote: Lys-326 is probably removed posttranslationally
A; Vote: Lys-326 is Probably removed posttranslationally
B; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
A; Reference number: A92809; MUID: 81007873; PMID: 6774012
A; Contents: myeloma protein Til
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F;239-306/Domain: immunoglobulin homology <IM3>
F;239-3106/Domain: immunoglobulin homology <IM3>
F;247-81/164 bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
Aritile: Disulphide bridges of the heavy chain of human immunoglobulin G2. A; Fitle: Disulphide bridges of the heavy chain of human immunoglobulin G2. A; Reference number: A0253; MUID:72033500; PMID:4940472
A; Contents: annotation; myeloma protein Sa, disulfide bonds
B; Frangione, B.; Milstein, C.; Pink, J.R.L.
A; Frangione, B.; Milstein, C.; Pink, J.R.L.
A; Title: Structural studies of immunoglobulin G.
A; Reference number: A93157; MUID:69064124; PMID:5782707
A; Contents: annotation; Sa, disulfide bonds
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A; Accession: A93132
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A,Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid A,Reference number: A90565, MUID:71064027; PMID:4923144
A,Cohrents: annoctation, disulfide bonds
R,Droker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A,Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob enbromide cleavage products, and the disulfide bridges.
A,Reference number: A91667; MUID:77070267; PMID:1002129
A,Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GDB:120085; OMIM:147100
A; Map position: 14q12.33-14q32.33
A; Map position: 14q12.33-14q32.33
A; Introns: 99/1; 114/1; 224/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin hemology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85/Domain: immunoglobulin homology < IMI>
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C;baceste: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J Blochen. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
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F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,25-308/Disulfide bonds: #steatus experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223
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A;Molecule type: mRNA
A;Moledues: 1-140, C', 142-374 <KH2>
A;Cssidues: 1-140, C', 1816-375
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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ilarity 91.8%; Pred. No. 1.9e-46;
Conservative 4; Mismatches 5;
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submitted to the EMBL Data Library, September 1994
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A;Cross-references: EMBL:X81695
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Matches 101; Conserv
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                                                                                                                                                                                                                                  Ig gamma-1 chain C region - human C;Species: Howe sapiens (man) C;Dpecies: Howe sapiens (man) C;Dpecies: Howe sapiens (man) C;Dpecies: Howe sapiens (man) C;Dpecies: Howe sapiens (man) C;Dpte: 31-Jan-1981 #Bequence revision 18-Aug-1982 #text change 09-Jul-2004 C;Accession: A93433; 836861; $33887; B90563; A90564; B91668; A91723; A02146 C;Accession: A93433; Breson, B.U.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433; MUID:8274238; PMID:6287432
A;Accession: A93433; MUID:8274238; PMID:6287432
A;Rosidues: 1-330 extlb.
A;Rosidues: UNIPROT:P01857; EMBL:217370
A;Note: this sequence has the GIm(17) allotypic marker, 97-Lys, and the GIm(1) markers, A;Note: Lys-330 is removed after translation
B;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Accession: Coscesion: Coscesi
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A, Residues: 88-113;235-330 < TAK>
A, Residues: 88-113;235-330 < TAK>
A, Cross. A. A. Cross. A. A. Surishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, B, A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, Biochemistry 9, 3161-3170, 1970
A, Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequent A; Reference number: A90563; MVID:71064024; PMID:5489771
A, Concents: myeloma protein Eu
A, Accession: B90563
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A; Residues: 1-34, 0', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Nothidt, WE.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des Kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A; Reference number: A91723; MUID: 83289131; PMID: 6884994
A; Contents: myeloma protein KOL; disulfide bonds
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A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgGl-Immunglobulins (Myelomprotein Nie),
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A; Readidues: 2-330 c4H2.
A; Readidues: 2-330 c4H2.
A; Cross-references: EMBL: 217370
B; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A; Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A; Reference number: S33887; MUID: 83001943; PMID: 6811139
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A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R.Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
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A;Readidues: 1-96, 'K',98-135 cCUN>
A;Note: this sequence has the Glm(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 317-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid
A;Reference number: A90564; MUID:71064025; PMID:5530842
              PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148
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A;Contents: myeloma protein Nie
A;Accession: B91668
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A,Residues: 1-96,'R',98-1
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Gyamma-3 heavy chain disease proteins - human
Cyamma-3 heavy chain disease proteins - human
Cyamma-3 heavy chain disease proteins - human
Cyaccession. 89442; A2219; A2199 #8equence revision 23-Oct-1981 #text_change 16-Jul-1999
Cyaccession. A90442; A2219; A20198; A91915; A01149
RyFrangione, B: Rosenwasser, E: Prelli, F: Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;fittle: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain disease protein Wis
A;foctents: heavy chain disease protein Wis
A;focte: the molecule type: protein
A;focte: the sequence of residues 42-76 was taken from the reference that follows
A;focte: the sequence of residues 42-76 was taken from the reference that follows
R;fichaelsen, T.E.; Frangione, B: Franklin, E.C.
A;focte: the sequence of residues 42-76 was taken from the reference that follows
R;fichaelsen, T.E.; Frangione, B: Franklin, E.C.
A;focte: the minany structure of the hinge region of human IgG3. Probable quadruplication
A;foctestion: A2219 wUID: 77118561; PMID:402363
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A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Molecule type: protein
A.Residues: 59-125,/EB'.128-226,228-289 «WOL»
A.Residues: 59-125,/EB'.128-226,228-289 «WOL»
A.Note: this protein lacks most of the V region, all of the CH1 region, and part of the
R.Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;
Proc. Natl. Acad. Sci. US.A. 79, 3260-3264, 1982
A.Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deletion
A.Reference number: A93915; MUID:82247835; PMID:6808505
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A,Map position: 14402.33-14432.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
E;203-270/Domalin: immunoglobulin homology <IMM>-
F;1703-270/Domalin: immunoglobulin homology <IMM>-
F;1704-270/Pomalin: immunoglobulin homology <IMM>-
F;1704-270/Pomalin: immunoglobulin homology <IMM>-
F;1704-270/Pomalin: are pyrrolidonydrate (Asn) (covalent) #status experimental
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Ig gamma 2b chain constant region - pig (fragment)
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Matches 96; Conserv
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A;Gene: GDB:IGHG3
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Cispecies: Accession: A23511
Rituck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
Airitle: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A; Accession: A23511
A; Reference number: A23511; MUID:86148507; PMID:3081877
A; Accession: A23511
A; Residues: 1-377 <HUC>
A; Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
Cigentics:
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A60764

G.Gorden C. region, form LAT - human
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C.JAccession: A60764
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221 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270
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A;Map position: 14q32.33-14q32.33
A;Intrans: 94/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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90.0%; Pred. No. 1.9e-45;
iive 4; Mismatches 7; Indels
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Pred. No. 1.9e-45;
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90.0%;
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Best Local Similarity
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Best Local Similarity
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A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 80.88
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 78.6
hes 81; Conservative
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               A; Accession: 147162
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A;Gene: IgG1
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Matches
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147159

19 gamma 2a chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C;Accession: 147159

R;Kacskovics, 1.; Suu, J.; Butler, J.E.

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147158; MUID:95015845; PMID:7930579
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Ig gamma 4 chain constant region - pig (fragment)
Ig gamma 4 chain constant region - pig (fragment)
Ig gamma 4 chain constant region - pig (fragment)
Ig gamma 5 constant domestica (domestic pig)
Is secons 12 constant domestica (domestic pig)
Is secons 147162
Is sequence revision 21-Feb-1997 #text_change 21-Jan-2000
Is secons 17 constant degree revision 21-Feb-1997 #text_change 21-Jan-2000
Is sequence 147162
Is sequence of the constant domestic pig sequences of the five putative subclasses of sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the constant domestic pig sequences of the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the f
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147160
R;Kacskovics, 1:, Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the CDNA sequences A;Title: Five putative subclasses of swine IgG identified from the CDNA sequences A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Accession: 147160
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
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llarity 81.7%; Pred. No. 2e-39;
Conservative 12; Mismatches 7; Indels
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A,Gene : 19G2b.
C,Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <1MM>
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81.7%; Pred. No. 2e-39;
ive 12; Mismatches
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Matches 85, Conservative
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Matches 85; Conserv
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R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: 147158; MUID:95015845; PMID:7930579
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R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: I47158; WUID:95015845; PMID:7930579
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C;Genetics:
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F;133-202/Domain: immunoglobulin homology <IMM>
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80.8%; Pred. No. 5.2e-39;
tive 12; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: 147161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.0%; Score 443; DB 2, 78.6%; Pred. No. 1e-36; live 12; Mismatches 1
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RESULT 15
C30554
Igh heavy chain C region - sheep (fragment)
Cj.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cj.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cj.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cj.Species: O. Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
Cj.Accession: C30554
R.Foley, R.C.; Bah, K.J.
J. Immunol. 142, 708-711, 1989
A.Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A.Reference number: A30554; MUID:89093962; PMID:2492052
A.Accession: C30554
A.Accession: C30554
A.Accession: C30554
A.Residues: 1-308 <FOL>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;113-182/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                               7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 66
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                                                                                              DB 2; Length 328;
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C;Superfamily: immunoglobulin C region; immunoglobulin homology F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                     Query Match 76.0%; Score 443; DB 2; Length 32 Best Local Similarity 78.6%; Pred. No. 1e-36; Matches 81; Conservative 12; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                    67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109
                                                                                                                                                                                                                                                                                                                                                                          176 NSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKA 218
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Search completed: November 17, 2005, 07:11:38 Job time : 19.0822 secs

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Q96pq8 1
Q6mzu6 1
Q6n096 P
Q65212 n
Q8nf17 P
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Q6mzx7
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                              protein search, using sw model
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GC753
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G6MZC7
GC2 HUMAN
GC2 HUMAN
GC6PX1
GC1 HUMAN
G6PX1
GC6PX1
GCGMX6
GC1 TO GCGMX6
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Q7Z351
Q6PJ95
Q96PQ8
Q6MZU6
Q6N096
Q6SZL2
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2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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Match Length DB
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P01868 mus musculu	GC1_MOUSE	Н	324	69.5	405	45
Q7tmk1 mus musculu	Q7TMK1	N	470	71.5	417	44
P03987 mus musculu	GC3M_MOUSE	-	398	71.5	417	43
P22436 mus musculu	GC3_MOUSE	-	329	71.5	417	42
Q6kam2 mus musculu	Q6KAM2	~	303	71.5	417	41
P01862 cavia porce	GC2_CAVPO	Н	329	73.1	426	40
P20761 rattus norv	GCB_RAT	-	333	74.3	433	39
P01870 oryctolagus	GC_RABIT	ч	323	74.3	433	38
Q95m34 equus cabal	Q95M34	~	337	79.2	462	37
P01860 homo sapien	GC3_HUMAN	Н	290	88.9	518	36
Q6n030 homo sapien	Q6N030	7	518	91.1	531	32
Q86tt2 homo sapien	Q86TT2	7	354	91.1	531	34
Q68cn4 homo sapien	Q68CN4	N	493	91.5	533.5	33
Q8n4y9 homo sapier	Q8N4Y9	N	521	91.6	534	36

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DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0005625; F:antigen binding; TAS.
DR GO; GO:0005655; P:immune response; NAS.
DR InterPro; IPR001301; Ig-like.
DR InterPro; IPR003006; Ig-MHC.
DR Ffan; PR0047; Ig: 3.
DR PRART; SM00407; IG: 12.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; Direct protein sequencing; Immunoglobulin C region; TM Immunoglobulin domain.
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MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=81157104; PubWed=6299662;
MEDLINE=81157104; Withouther J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
                                                                                                                                                                                                                                         21-JJJ-1986 (Rel. 01, Created)
21-JJJ-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Iggamma-4 chain C region.
                                                                                                                                                                              327 AA
ALIGNMENTS
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PIR; A90933; G4HU.
PDB; 1ADQ; X-ray; A=118-323;
Genew; HGNC:5528; IGHG4.
MIM; 147130; -.
                                                                                                                                                                          PRT;
                                                                                                                                                                              STANDARD;
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                                                                                                                                                                      GC4_HUMAN
P01861;
                                                                                                                                 | ACCC | HUMAN | ACCC | HUMAN | ACCC | HUMAN | ACCC | BULKAR | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | ACCC | AC
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NCBI_TaxID=9606;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Natusner R.D., Colling F.S., Wagner L., Shemenc C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hosph R.N.,
A Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton B., Ketterman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Muhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Makray M., Touchman J.W., Green E.D., Dickson M.C.,
Jones A.C., Gaimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                            Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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CH3.
Interchain (with a light chain).
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(with a heavy chain)
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                       35940 MW; 3EDBD811EF208E7A CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                            0; Mismatches
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InterPro; IPR000923; Bluecu 1.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
Pfam; PF07654; Cl. set; 3.
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Matches 107; Conservative
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327 AA;
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TISSUE=Kidney;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                Length 473;
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Pred. No. 1.2e-47;
1; Mismatches 3; Indels
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SMART; SM00406; IGV; 1.
PROSITE; PS00196; COPPER BLUE; UNKNOWN_1.
PROSITE; PS00035; IG_LIKE; 4.
PROSITE; PS000290; IG_MHC; UNKNOWN 3.
SEQUENCE 473 AA; 51986 MW; E29920B09BA369FS CRC64;
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                                                                                                                           Query Match 96.9%; Score 565; DB 2; Lv
Best Local Similarity 97.3%; Pred. No. 5.9e-48;
Matches 107; Conservative 0; Mismatches 3;
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PROSITE; PS00239; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 476 AA; 52420 WW; 0D3D1F
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05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
Hypothetical protein DKFZp686M24218.
Name=DKFZp686M24218;
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P01859;
21-JUL-1986 (Rel. 01, Created)
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Matches 106; Conservative
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Frangione B., Milstein C., Pink J.R.L.; "Structural studies of immunoglobulin G."; Nature 221:145-148(1969).
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35884 MW;
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SMART; SM00407; 1GC1; 2.
PROSITE; PS0835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
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Conservative
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HSSP; P01857; 10QX.
Genew; HGNC:5526; IGHG2.
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Matches 103; Conserv
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MEDLINE=84235992; PubMed=6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma
                                                                                                                                                                                                                       Ellison J.W., Hood L.E.;
"Linkage and sequence homology of two human immunoglobulin gamma heavy
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MEDLINE=83001943; PubMed=6811139; DOI=10.1016/0092-8674(82)90183-0;
Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
Cell 29:671-679(1982).
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MEDLINE=80001357; PubMed=113060;
Connell G.E., Parr D.M., Hofmann T.;
The amino acid sequences of the three heavy chain constant region domains of a human 1962 myeloma protein.";
Can. J. Blochem. 57:758-767(1979).
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MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9; Hofmann T., Parr D.M.;

A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";

Mol. Immunol. 16:923-925(1979).
                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
MEDLINE=81007873; PubMed=6774012;
Wang A.-C., Tung E., Fudenberg H.H.;
"The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
                                                                                                                                                                                                                                                                 chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
21-JUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Ig gamma-2 chain C region.
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Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
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MEDLINE=69064124; PubMed=5782707;
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                                                                                  Homo sapiens (Human)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 169
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S -> A (in myeloma proteins TIL and ZIE)
FyrId-VARA 003889.
C -> S (in Ref. 3).
8310878C6878CF9C CRC64;
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05-UTL-2004 (TrEMBLrel. 27, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686I04196 (Fragment).
Name-DKFZp686I04196;
Name-DKFZp686I04196;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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heavy
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NON TER 1 1 10 CH1.

DOMAIN 99 110 Hinge.

DOMAIN 111 219 CH2.

DOMAIN 220 326 CH3.
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93.6%; Pred. No. 6.9e-46;
iive 3; Mismatches 3
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SEQUENCE FROM N.A.
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P01857;
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Lapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Nitlanon D.K., Muzny D.M., Sodergren B.J., Lu X., Glübs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

R Jones S.J., Marra M.A.;

R Jones S.J., Marra M.A.;

R Jones S.J., Marra M.A.;

R R Generation and initial analysis of more than 15,000 full-length human
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                                                                    TISSUE=Human esophagus tumor;

THE German Human cDNA Consortium;

Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Fobo G., Han M., Wiemann S.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640623; CAB45777.1; --

HSSP; P01861; 1ADQ.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Last annotation update)
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InterPro; IPR003599; IG.
InterPro; IPR003597; IG_C1.
InterPro; IPR003597; IG_C1.
InterPro; IPR003596; IG_MHC.
InterPro; IPR003596; IG_N.
InterPro; IPR003596; IG_N.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 3.
PR03ITE; PS50835; IG_LIKE; 3.
PR03ITE; PS50835; IG_LIKE; 3.
PR03ITE; PS60290; IG_MHC; UNKNOWN_2.
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  NCBI_TaxID=9606;
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250 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 308
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.
Waxdal M.J., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                               Strausberg R., Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 AA; 51325 MW; FDDB9348ADC37E6D CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 542.5; DB Pred. No. 1e-45;
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21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
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INTERPRO; IPR003599; IG.
INTERPRO; IPR003599; IG-like.
INTERPRO; IPR003597; IG-like.
INTERPRO; IPR003597; IG-like.
INTERPRO; IPR003596; IG-MHC.
INTERPRO; IPR003596; IG-MHC.
PRART; SM00409; IG; 2.
SWART; SM00409; IG; 2.
SWART; SM00406; IGC; 3.
PROSITE; PS50835; IG-LIKE; 4.
PROSITE; PS50835; IG-LIKE; 4.
PROSITE; PS50835; IG-LIKE; 4.
PROSITE; PS60830; IG-MHC; UNKNOWN_2.
Hypothetical protein.
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SEQUENCE FROM N.A.
MEDLINE-82274238; PubMed-6287432;
Ellison J.W., Berson B.J., Hood L.E.;
Ellison J.W., a sequence of a human in "The nucleotide sequence of a human in "The nucleotide sequence".
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MEDLINE=77070269; Pubmed=826475;
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Best Local Similarity 93.6%;
Matches 103; Conservative
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N-linked (GlcNAc. . .).
K -> R (in GlM(3) marker).
/FTId=VAR 003886.
D -> E (in GlM(non-1) marker).
FTId=VAR 003887.
L -> M (in GlM(non-1) marker).
/FTId=VAR_003889.
                                                                                                                                                                                                                                          (with light chain)
(with heavy chain)
(with heavy chain)
                                                                                                   GO; GO:0005624; C:membrane fraction; NAS. GO:0003823; F:antigen binding; TAS. GO: GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
          PDB; 2RCS; X-ray; H=1-103.
Genew; HGNC:5525; IGHG1.
MIM; 147100; -.
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103
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Ponstingl H., Hilschmann N.;

"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";

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                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
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                                                                                           SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
MEDLINE=83289131; PubMed=6884994;
Schmidt W.E., Unng H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: KOL also differs in the amidation states of
                                                                                                                                                                             DISULFIDE BONDS.

MEDLINE=71064027; PubMed=4923144;

Gall W.E., Edelman G.M.;

"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";

Biochemistry 9:3188-3196(1970).
                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS)
MEDLINE=81208100; PubMed=7236608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, J00228; AAC82527.1; ALT_INIT.
PTR, A3343; GHHU
PDB; IAJ7, X-ray; H=1-101.
PDB; IDSI; X-ray; H=1-101.
PDB; IDSI; X-ray; H=1-101.
PDB; IDSI; X-ray; H=1-101.
PDB; IDSI; X-ray; H=1-101.
PDB; IDSI; X-ray; H=1-101.
PDB; IDSI; X-ray; A/B=106-329.
PDB; IPCJ; X-ray; A/B=106-329.
PDB; IFCJ; X-ray; A/B=106-329.
PDB; IFCJ; X-ray; A/B=106-329.
PDB; ITCJ; X-ray; B/D=1-103.
PDB; ITZ; X-ray; B/D=1-103.
PDB; ITZ; X-ray; A/B=107-330.
PDB; ITX; X-ray; A/B=107-330.
PDB; IUX; X-ray; A/B=107-330.
PDB; IUX; X-ray; A/B=107-330.
PDB; IOX; X-ray; A/B=119-330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residues 198, 267 and 272.
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268-272

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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=124.7932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=124.7932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=124.7932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=124.7932; MEDLINE G.D.,

MEDLINE=22388257; Medline F.S., Marcher A., Rubin G.M., Helph F.,

MEDLINE=228882 M., McDline T.B., Toshiyuki S., Carninori P., Prange C.,

MEDLINE=228882 M., McDline T.B., McDline M.J., Abramson R.D., Mullahy S.J.,

MEDLINE=228882 M., McDline F.S., McDline F.S., Marcher M.J., Maden A., Gunaratne P.H.,

Milalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Milalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Milang M., Touchman J.W., Maden A., Rodrigues S., Sanchez A.,

Milang M.J., Touchman J.W., Green B.D., Dickson M.C.,

Medriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Medliguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Medliguez A.C., Marra M.A.,

Medliguez M.D., Medliguez M.D., Medliguez M.D., Marra M.A.,

Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D., Medliguez M.D.
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                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Name=IGHG1,
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 358
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Pred. No. 1.5e-45;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB=Primary B-Cells;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH73766.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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InterPro; 1PR003599; 19.
InterPro; 1PR003597; 19.
InterPro; 1PR003507; 19.
InterPro; 1PR003506; 19.
MHC.
InterPro; 1PR003506; 19.
Pfam; PP00464; C1-set; 3.
Pfam; PP0047; 19; 4.
SMART; SM00409; 1G; 2.
SMART; SM004009; 1G; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.8%;
Matches 101; Conservative
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences."
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465 AA; 5
         sapiens (Human)
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                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                 Length 330;
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                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhu N.S., Chen Y.Y.;
Submitted (MAR-2204) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS70731; AAS88328.1; -.
HSSP; P01857; 1AJ7.
                                                                                                                                                                36106 MW; 3770EE106C2FA33D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 AA; 38162 MW; DD96C3D7E0BE5845 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hepatitis B virus receptor binding protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                            92.8%; Score 541; DB 1;
llarity 91.8%; Pred. No. 9.9e-46;
Conservative 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 541; DB 2;
Pred, No. 1.1e-45;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam, PF07054; Cl-set; 3.
SMART; SW00407; IG_LIKE; 3.
PROSITE; PS00290; IG_LIKE; UNKNOWN_2.
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(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
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05-JUL-2004 (TrEMBLrel
05-JUL-2004 (TrEMBLrel
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                              330 AA;
                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                     Matches 101;
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NON TER
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                                                                                                                                                              SEQUENCE
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Best Local
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RESULT 9 Q6GMX6

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SEQUENCE FROM N.A.
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                                TISSUB-PETIPHERAL Nervous System;

TISSUB-PETIPHERAL Nervous System;

TISSUB-PETIPHERAL Nervous System;

MEDLINE-2238257; PubMed-1247932; DOI=10.1073/pnas.242603899;

Katausherg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Astapleron M., Soares M.B., Bonaldo M.F., Carannor P.D., Hsieh F.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunzaren P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabay J., Helton B.K., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Norley W., Salska U., Schmutz J., Myers R.M., Butcerfield Y.S.,

Norley W., Marra M.J.,

Jones S.J., Marra M.J.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 466;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 541; DB 2; Length 46
Pred. No. 1.5e-45;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Peripheral Nervous System;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 466 AA; GOBS3 MW; 53EB0BCEDE81076E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, BC072419; AAH72419.1;
HSSP; P01861; 1ADQ.
INCEMPRO; IPR007110; Ig.
INCEMPRO; IPR007110; Ig.-like.
INCEMPRO; IPR003097; Ig.-like.
INCEMPRO; IPR003006; Ig_MHC.
INCEMPRO; IPR003096; Ig_WHC.
INCEMPRO; IPR003096; Ig_WY.
Pfam, PPF054; C1-8et; 3.
SWART; SW00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 92.8*;
Best Local Similarity 91.8*;
Matches 101; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7Z/P5;
01-0CT-2003 (TrEMBLrel. 25,
01-0CT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Caraninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Halton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Multing M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
C., Shevchenko Y., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.,
C., Ganerrain and initial analysis of more than 15,000 full-length human
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TISSUB-Primary B-Cells,
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RBBL; BC051328; AAH51328.1; -.

RBSP; PO1857; 1HZH.

InterPro; IPR00110; Ig-like.

InterPro; IPR003597; Ig_c1.

InterPro; IPR003506; Ig_WHC.

InterPro; IPR00406; Ig_W.

RART; SM00406; IGy. 1.

RPC051TE; PS50835; IG_LIKE; 4.

RPC051TE; PS50835; IG_LIKE; 4.

RPC051TE; PS00290; IG_MHC; UNKNOWN 2.

SEQUENCE 469 AA; 51395 MW; CBD5BE12BAAF795C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 469;
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91.8%; Pred. No. 1.5e-45;
ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
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Best Local Similarity 91.83
Matches 101;· Conservative
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SEQUENCE
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Q6N089
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues R.S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A., Green E.D., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Spleen;
TISSUE=Spleen;
TISSUE=Spleen;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buederow K.H., Scheefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                        Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018747; AAH18747.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                       InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003597; IG_C1.
InterPro; IPR003597; IG_MHC.
InterPro; IPR003595; IG_WHC.
InterPro; IPR003595; IG_WHC.
InterPro; IPR003595; IG_WHC.
InterPro; IPR003595; IG_WHC.
INTERPROSERT; SW004009; IG_Y; IG_LIKE; A.
PROSITE; PS00359; IG_LIKE; 4.
PROSITE; PS00395; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 91.8
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                HSSP; P01861; 1ADQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Q725W1;
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313
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villahon D.K., Nuzny D.D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGGPSVFLFPPKFDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Human rectum tumor;
The German Human cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausbeig R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO53984; AAH53984.1; -.
HSSP; P01867; HZH.
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640627; CAE45781.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.8%; Score 541; DB 2; Le 91.8%; Pred. No. 1.5e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
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Name=DKFZp686P15220;
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InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; Pr07654; C1-eet; 3.
SMART; SM00406; IGv; 1.
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InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; Cl-set; 3.
SWART; SM00409; IG; 2.
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Matches 101; Conservative
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TISSUE=Spleen;
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                                                                                                                                                                                                                                                                                                                                256 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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Vertebrata; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                61 PREEQFNSTYRVVSVLTVLHODWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 365
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                                                                                                                                                                      Query Match 92.8%; Score 541; DB 2; Length 472; Best Local Similarity 91.8%; Pred. No. 1.5e-45; Matches 101; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 92.8%; Score 541; DB 2; Length 473; Best Local Similarity 91.8%; Pred. No. 1.5e-45; Matches 101; Conservative 4; Mismatches 5; Indels
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein DKFZp686C11235.
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AC Q6MZV7
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November 17, 2005, 06:51:22 ; Search time 24.6119 Seconds (without alignments) 333.636 Million cell updates/sec
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Sequence 47, 2
Sequence 12, 7
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-968-362A-28

US-08-761-277A-47

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OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure 2 OTHER INFORMATION: B) APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill
APPLICANT: Sun, Bill
APPLICANT: Sun, Bill
APPLICANT: Sun, Bill
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: For fusion proteins of human granulocyte colony-stimulaing factor
TITLE OF INVENTION: increased biological activities
FILE REFERENCE: 03SUN2001
CURRENT PELING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 449 ö 9 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK DIAGNOSTIC AGENT Gaps Sequence Seq 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 ö 293 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK Length 449 Indels US-08-444-644-44

Sequence 44, Application US/08444644

Sequence 44, Application US/08444644

Sequence 44, Application US/0844644

Parent No. 6015555

TITLE OF INVENTION: Phillip M.

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAC

TITLE OF INVENTION: CONJUGATES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS: 46

STREET: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive Query Match 97.8%; Score 570; DB 4; L Best Local Similarity 98.2%; Pred. No. 2.2e-60; Matches 108; Conservative 0; Mismatches 2; US-08-595-590B-26 US-08-595-590B-28 US-09-968-362A-22 US-09-968-362A-18 US-09-485-737B-67 US-09-499-846-12 US-09-499-846-12 US-09-499-846-10 US-09-499-846-10 US-09-499-846-10 US-09-499-846-10 US-09-499-846-10 US-09-499-846-10 US-09-485-30 US-09-485-30 US-08-232-246A-30 US-09-483-588-5 US-09-968-362A-27 US-08-477-460B-2 US-08-379-516-2 US-09-329-916-2 ALIGNMENTS US-09-968-362A-20 ; Sequence 20, Application US/09968362A : Patent No. 6797493 ; GENERAL INFORMATION: TYPE: PRT ORGANISM: Artificial Sequence US-09-968-362A-20 ठ 임 ò g

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1 APEFLGGPSVFLFPPKPXDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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Patent No. 6737056
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: Polypetide Variants with Altered Effector Function
FILE REFERENCE: P1726R1
CURRENT APPLICATION NUMBER: US/09/483,588
CURRENT FILING DATE: 2000-01-14
EARLIER FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 7
LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentln Belease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-52P-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-52P-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-52P-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REFERENCE/DOCKET NUMBER: 34-480
REFERENCE/DOCKET NUMBER: 34-480
REFERENCE/DOCKET NUMBER: ALKBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
96.9%; Score 565; DB 3;
Best Local Similarity 97.3%; Pred. No. 1.3e-60;
Matches 107; Conservative 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 110 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 97.3
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-232-246A-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-09-483-588-7
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US-08-232-246A-44

i Sequence 44, Application US/08232246A

j Sequence 47, Explication US/08232246A

general No. 6329508

deneral INFORMATION:
    TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

TITLE OF INVENTION: CONJUGATES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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Pred. No. 1.3e-60;
0; Mismatches 3; Indels
                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                              PRIOR APPLICATION 124
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US 07/800/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1999
ATTONNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: ALK88-15AAAZ
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR EXECTION NUMBER: (617) 861-9540
INFORMATION FOR EXECTION NUMBER: (617) 861-9540
INFORMATION FOR EXECTION NUMBER: (617) 861-9540
                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.9%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 110 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 97.33
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
     Lexington
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                                                  USA
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                                    FILING DATE:
                                                                      02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                  COUNTRY:
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Gaps

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1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09313942

Sequence 12, Application US/09313942

Setent No. 6472179

GENERAL INFORMATION:

APPLICANT: REGENEROR PHARMACEUTICALS, INC.

TITLE OF INVENTION: AND USING

FILE REFRENCE: REG 203-4

CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT APPLICATION NUMBER: 09/313,942

PRIOR APPLICATION NUMBER: 60/113,942

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 12

LEGISTOR FOR SEQ ID NOS: 32

SEQ ID NO 12

LEGISTOR FOR SEQ ID NOS: 32

SEQ ID NO 12
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                                                                                                                                                                                       Length 327;
                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                       Score 565; DB 2;
Pred. No. 5.9e-60;
0; Mismatches 3;
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APPLICANT: Browne, Michael J.
APPLICANT: Murphy, Kay E.
APPLICANT: Chapman Conrad G.
APPLICANT: Clinkenbeard, Helen E.
APPLICANT: Shatzman, Allan R.
APPLICANT: Shatzman, Allan R.
TITLE OF INVENTION: No. 5783181e1 Compounds
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/08470299
; Patent No. 5783181
       47:
                                                                                                                                                                                          Query Match 96.9%;
Best Local Similarity 97.3%;
Matches 107; Conservative
  INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 96.9
Best Local Similarity 97.3
Matches 107; Conservative
                                                                                                                 , MOLECULE TYPE: protein US-08-761-277A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                    linear
                                                                                               TOPOLOGY:
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US-08-470-299-7
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                                                                                                                                                                                                                               APPLICANT: Sun, B111
APPLICANT: Sun, B111
APPLICANT: Sun, B111
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: For fusion proteins of human granulocyte colony-stimulaing factor TITLE OF INVENTION: increased biological activities
FILE REFERENCE: 038UN2001
CURRENT APPLICATION NUMBER: US/09/968,362A
CURRENT FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Human 1964 Fc with native hinge, CH2 and CH3 domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 47, Application US/08761277A
Patent No. 597234
GENERAL INFORMATION:
APPLICANT: Denney Jr., Dan W.
TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
TITLE OF INVENTION: Leukemia
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 565; DB 4; Length 229;
Pred. No. 3.6e-60;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: RADABLE FORM:

MEDIUM TYPE: RADABLE FORM:

MEDIUM TYPE: RADABLE FORM:

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: PACENTIN Release #1.0, Version #1.30

SOFTWARE: PACENTIN Release #1.0, Version #1.30

RPLICATION NUMBER: US/08/761,277A

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/644,664

FILING DATE: UD 1-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: MACKINGH, RAMIN T.

REGISTRATION NUMBER: 38.230

REFERENCE/DOCKET NUMBER: GENITOPE-02406

TELEPHONE: (415) 705-8410

TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
                                                                                                                                       Sequence 28, Application US/09968362A, Patent No. 6797493
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 97.3%;
Matches 107; Conservative
                                                                                                                   US-09-968-362A-28
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US-08-761-277A-47
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SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
        P31005C3
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
REFERENCE/DOCKET NUMBER: P31(
TELECHMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELERAX: 610-270-5030
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 805 Third Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   Best Local Similarity 97.3
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                   ; TOPOLOGY:
US-08-470-299-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US96-13152-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: N
STATE:
                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 96.9%; Score 565; DB 1; Length 382; Best Local Similarity 97.3%; Pred. No. 7.3e-60; Matches 107; Conservative 0; Mismatches 3; Indels
                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,299
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SULTON, JG.F.F.Y A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P11005C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEPHONE: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentUn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,299
FILING DATE: 06-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Browne, Michael J.
APPLICANT: Murphy, Kay E.
APPLICANT: Chapman, Conrad G.
APPLICANT: Clinkenbeard, Helen E.
APPLICANT: Young, Peter R.
APPLICANT: Sharzman, Allan R.
TITLE OF INVENTION: No. 5783181el Compounds
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: SmithKline Beecham Corporation 709 Swedeland Road, P.O. Box 1539
                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08470299
Patent No. 5783181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: SULton, Jeffrey A.
REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 382 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        King of Prussia
  King of Prussia
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                      Pennsylvania
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-470-299-7
                                                                 19406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Kir
STATE: PE
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-08-470-299-10
                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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pCT-US96-13152-4

Sequence 4, Application PC/TUS9613152

GENERAL INFORMATION:

APPLICANT: Martin, Ulrich, et al.

TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

ADDRESSEE: Attn: Norman D. Hanson
                                                                                                                                                  166 APEFEGGPSVFLFPPRDYDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 225
                                                                                                                1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                            0; Gaps
                                                                                                                                                                                                                           61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                             226 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 275
96.9%; Score 565; DB 1; Length 382; 97.3%; Pred. No. 7.3e-60; Ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTONEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.9%; Score 565;
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Sequence 45, Application US/07916098A
Patent No. 5871722
GENERAL INFORMATION:
APPLICANT: THOMAS, DAVID W.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, WARGARET D.
APPLICANT: ROSA, WARGARET D.
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETII & WITHOUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.9%; Score 565; DB 2; Length 467; 97.3%; Pred. No. 9.5e-60; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COPERATING SYSTEM: PC COMPATIBLE WORD PERFECT 5.1

CURRENT APPLICATION DATA: Flind DATE: July 24, 1992
CLASSIFICATION WUMBER: DCT/US91/08843

PRIOR APPLICATION DATA: A24

PRIOR APPLICATION 1424

PRIOR DATE: NO. 5871732ember 27, 1991
CLASSIFICATION: 424

APPLICATION NUMBER: 07/618,542

FLING DATE: NO. 5871732ember 27, 1990
CLIASSIFICATION: 424

ATTORNEY AGENT INFORMATION: NUMBER: JOHN J. MC DONNELL
                                                                                                                                                                                                                                                                                                                                        STREET: 10 SOUTH WACKER DRIVE CITY: CHICAGO STATE: LILINOIS COUNTRY: U.S.A. ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELER: 910/221-5317
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08523894
Patent No. 6136310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 96.9
Best Local Similarity 97.3
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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Patent No. 570514

GENERAL INFORMATION:
APPLICANT: Dalie, Barbara
APPLICANT: Miler, Kenneth
APPLICANT: Miler, Kenneth
APPLICANT: Miler, Kenneth
APPLICANT: Micholas
APPLICANT: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
                                                                                                                                         251 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYVDGVEVHNAKTK 310
                                                                                                          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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                                                            0; Gaps
                                                                                                                                                                                                            61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                           287 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 96.9%; Score 565; DB 1; Length 467; Best Local Similarity 97.3%; Pred. No. 9.5e-60; Matches 107; Conservative 0; Mismatches 3; Indels
                                                          3; Indels
                                  Pred. No. 8.9e-60;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh COMPUTER: Apple Macintosh COMPUTER: Apple Macintosh 7.5.3 SOFTWARE: Microsoft Word 5.1a CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/704,744 FILING DATE: 06-SEPT-1996 CLASSIFICATION DATA: US/08/20886 FILING DATE: 10-MAR-1994 APPLICATION NUMBER: PCT/US/95/02400 FILING DATE: 08-MAR-1995 ATTORNEY/ACBNT INFORMATION: NAME: FOUlke, Cynthia L. REGISTRATION NUMBER: J3,364 REFERENCE/DOCKET NUMBER: UB0429K TELECOMMUNICATION:
                                  97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (908) 298-2987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (908) 298-5388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                               Best Local Similarity 97.3
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Kenilworth
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                   US-08-704-744-81
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Score 565; DB 3;
Pred. No. 9.5e-60;
                                                                                              012712-165
  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-6220
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acids
                                                                     35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.98;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                 linear
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Best Local Similarity
                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                            US-08-523-894-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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US-08-523-894-10
is Sequence 10, Application US/08523894
js Patent No. 6136310
is GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
  Recombinant Anti-CD4 Antibodies for Human Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 96.9%; Score 565; DB 3; Length 467; Best Local Similarity 97.3%; Pred. No. 9.5e-60; Matches 107; Conservative 0; Mismatches 3; Indels
                                                                                                                                                               CUUNTER: VA

ZIP: 22314-3187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAETHLIN Release #1.0, Version #1.30

CUBRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/523,894

FILING DATE: 06-SEP-1995

CLASSIFICATION: 424

ATTORNEY AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-165

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: 05-68P-1995
TITLE OF INVENTION: Recombinant Anti-CD4 Ant
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: BURNS, DOANE, SWECKER & MATHIS
F: 699 Prince Street
Alexandria
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-523-894-8
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1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08523894

Patent No. 6136310

GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CONTY: ALEXANDARIA
                                                                                                                                                                                                                                          61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                  311 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 360
Query Match 96.9%; Score 565; DB 3; Length 467; Best Local Similarity 97.3%; Pred. No. 9.5e-60; Matches 107; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: USA
ZIP: 103A
ZIP: 22314-3187
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOEDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
RELECOMMULCATION INFORMATION:
TELEPHONE: 703-835,030
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Matche	3 10	, 70	Matches 107; Conservative	, 0	0; Mismatches	3;	3; Indels	; 0	0; Gaps	.; 0
ò	7	API	1 APPVAGGESVFLFPPKFKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60	TLM	ISRTPEVTCVVVDVS	OEDE	EVOFNWYVDC	SVEVE	INAKTK	09
Dp	251	APE	251 APEFEGGESVFLEPPKPKDTLMISRTPEVTCVVDVSQEDPEVQFNWYVDGVEVHNAKTK 310	TI I		OEDE	EVQFNWYVDC	3VEV	INAKTK	310
ò	61	PRE	61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKCLPSSIEKTISKAK 110	HODY	ALNGKEYKCKVSNKG	LPSS	IEKTISKAK	110		
qa	311	PRE	311 PREEQFINSTYRVUSULTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 360	-QH	VLNGKEYKCKVSNKO	LPS	IEKTISKAK	360		
o dores	واسير	4	Search completed. November 17 2005 07:13:22	5	22.13.22					

Search completed: November 17, 2005, 07:13:22 Job time : 24.6119 secs

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November 17, 2005, 07:05:08; Search time 84.3836 Seconds (without alignments) 545.427 Million cell updates/sec
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GenCore version 5.1.6 · Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1867879 seqs, 418409474 residues
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

UMMARIES	1111111111
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	:	9, Appli	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
;	10	US-10-959-318-9	US-10-959-318-10	US-11-018-102-25	US-09-932-812-20	US-10-761-593A-20	US-11-016-518A-20	US-11-017-185-20	US-09-968-362-20	US-10-800-497-20	US-10-800-449-20	US-10-006-593-67
		18	18	20	10	16	50	50	10	16	16	14
å Query	Length	110	110	110	437	437	437	437	449	449	449	472
Query	Match	98.8	98.3	97.9	97.8	97.8	97.8	97.8	97.8	97.8	97.8	97.2
Ċ	score	576	573	571	570	570	570	570	570	570	570	566.5
Result		7	8	m	4	ß	Q	7	60	6	10	11

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US-10-307-724-6 US-10-737-290-6 US-10-959-318-4 US-11-018-102-2 US-09-813-341-5	10-196-394- 10-370-749- 10-835-642- 10-757-863- 10-982-470- 11-158-839-	US-10-761-593A US-10-800-497A US-11-016-518A US-11-016-518A US-11-017-1854 US-11-017-1854	15 US-10-433-108-24 0 US-09-925-664-47 11 US-09-925-192-47 13 US-10-047-542-26 14 US-10-310-719-7 14 US-10-112-582-4	10-822-300-10-822-300-10-822-300-10-891-972-10-891-972-10-982-359-10-982-359-10-937-596-1
472 472 110 110 218	218 218 218 218 218	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	284 327 327 327	3888 3888 3887 788 888 788 788 788 788 7
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113	18 20 22 23 23	3 2 2 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		, w w 4 4 4 4 4 6 8 9 0 4 6 6 6 6 7

ALIGNMENTS

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RESULT INFORMATION: US20050215768A1

Sequence 9, Application US/10959318

Sequence 9, Application WS/10959318

Sequence 9, Application WS/10959318

GENERAL INFORMATION: Wichael R

TITLE OF INVENTION: Polypeptides including modified constant regions

TITLE OF INVENTION: POlypeptides including modified constant regions

FILE REFERENCE: 39-302

CURRENT APPLICATION UNMBER: PCT/GB2004/004254

PRIOR APPLICATION UNMBER: PCT/GB2004/004254

PRIOR APPLICATION UNMBER: PCT/GB2004/004254

PRIOR FILING DATE: 2004-10-07

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTION: Variant of Human IgG1 CH2 sequence with delta a, c and d (D268)

TYPE: PT

ORGANISM Artificial Sequence

FRATURE:

OTHER INFORMATION: Wutations

US-10-999-318-9

Query Match

APPLAGESPERPERPETATION: Wimmatches 0; Indelta 0; Gaps 0;

MATCHES 108; CORSETVATIVE: 0; Mismatches 0; Indelta 0; Gaps 0;

APPLAGESPERPETATION: Wimmatches 0; Indelta 0; Gaps 0;

APPLAGESPETATION: Wimmatches 0; Indelta 0; Indelta 0; Indelta 0; Indelta 0; Indelta 0; Indelta 0; Indelta 0; Indelta 0; Indelta 0; Indelta 0; Indelta 0; Indelta 0; Indel
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US-09-32-812-20
Sequence 20, Application US/0932812
Sequence 20, Application US/0932812
Sequence 20, Application US/0932812
Sequence 20, US20330882749A1
Sequence 20, US20330882749A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Cecily R
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biologic CURRENT APPLICATION NUMBER: US/09/932,812
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 437
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide (Figure 2B ; OTHER INFORMATION: )
US-09-932-812-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-761-593A-20

Sequence 20, Application US/10761593A

Publication No. US20040175824A1

GENERAL INFORMATION:

APPLICANT: Sun, Blll N

APPLICANT: Sun, Blll N

TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological

TITLE OF INVENTION: activities
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   61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Best Local Similarity 98.2%; Pred. No. 7.2e-47;
Matches 108; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.8%; Score 570; DB 16; 98.2%; Pred. No. 7.2e-47; iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 025UN2011-A
CURRENT APPLICATION NUMBER: US/10/761,593A
CURRENT FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 09/932812
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.2
Matches 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Variant of Human 1gG1 CH2 sequence with delta a, c and e (E268)
OTHER INFORMATION: mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/11018102
PUblication No. US20050136061A1
GENERAL INFORMATION:
APPLICANT: Centcoor. inc.
TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN5045 USA NP
CURRENT FILING DATE: 2004-12-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                              APPLICANT: Clark, Michael R
APPLICANT: Clark, Michael R
TILE OF INVENTION: PolyPeptides including modified constant regions
FILE REFERENCE: 39-302.
FILE REFERENCE: 30-302.
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: PCT/GB2004/004254
PRIOR APPLICATION NUMBER: GB0324368.0
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
SECTUAL OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATEN
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                                  PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Pred. No. 7.7e-48;
3; Mismatches 0;
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OTHER INFORMATION: engineered G4 CH2
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US-10-959-318-10
; Sequence 10, Application US/10959318
; Publication No. US20050215768A1
; GENERAL INFORMATION:
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Best Local Similarity 97.3%;
Matches 107; Conservative
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Best Local Similarity 98.2
Matches 108; Conservative
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ORGANISM: Artificial
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US-11-018-102-25
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LENGTH: 110
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PEATURE:
OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure 2 OTHER INFORMATION: B)
US-09-968-362-20
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Publication No. US20030082679A1
Publication No. US20030082679A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: For fusion proteins of human granulocyte colony-stimulaing factor TITLE OF INVENTION: biological activities
FILE REFERENCE: 035UN2001
CURRENT APPLICATION NUMBER: US/09/968,362
CURRENT APPLICATION NUMBER: 2011-10-30
UNDER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
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                                                                        233 APEFAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 292
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publication No. US20040259209A1

general information:

GENERAL INFORMATION:

APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Lee-Hwei K

TITLE OF INVENTION: Cecily R

TITLE OF INVENTION: Etimulaing factor with

TITLE OF INVENTION: stimulaing factor with

TITLE OF INVENTION: increased biological activities

FILE REFERENCE: 035UN2001

CURRENT APPLICATION NUMBER: US/10/800,497

CURRENT FILING DATE: 2004-03-15

PRIOR PEPLIANG DATE: 2001-10-01

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.1

SEQ ID NO 20

LENGTH: 449
                                                 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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  Gaps
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                                                                                                                                                61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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  Indels
  0; Mismatches
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Matches 108; Conservative
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Sublication No. US20050142642Al

Sublication No. US20050142642Al

GENERAL INFORMATION:

APPLICANT: Sun, Dee-Hwei K

APPLICANT: Sun, Cecily R

TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biologi

TITLE OF INVENTION: Activities

TITLE OF INVENTION: Activities

FILE REFERENCE: 025UN2001D2

CURRENT APPLICATION NUMBER: US/11/017,185

CURRENT FILING DATE: 2004-12-17

PRIOR PLING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.1

SEQ ID NO 20

LENGTH: 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide (Figure; OTHER INFORMATION: 2B)
US-11-016-518A-20
                                                                                                                                                                                     Sequence 20, Application US/11016518A
Publication No. US20050124045A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Eall N
APPLICANT: Sun, Eall N
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: FC fusion proteins of human erythropoietin with increased
TITLE OF INVENTION: biological activities
TITLE OF INVENTION: biological activities
CURRENT APPLICATION NUMBER: US/11/016,518A
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US 09/932,812
PRIOR APPLICATION UNDER: US 09/932,812
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.2
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Pred. No. 7.2e-47;
0; Mismatches 2;
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Pred. No. 7.2e-47;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 98.29
Matches 108; Conservative
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Best Local Similarity
                                                                                                                                                                        -11-016-518A-20
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LENGTH: 437
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257 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 315
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                                                                                                                                                                                                                                                               Score 566.5; DB 14; Length 472;
Pred. No. 1.7e-46;
0; Mismatches 0; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 67, Application US/10307724
Publication No US20030232972A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
TILLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REPERENCE: 1087-2cip
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-39
PRIOR FILING DATE: 2001-05-36
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO S: 134
                                                                                                                                                        FEATURE:
; OTHER INFORMATION: Humanized antibody heavy chain
US-10-006-593-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Humanized antibody heavy chain US-10-307-724-67
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                           SOFTWARE: Patentin version 3.1
SEQ ID NO 67
LENGTH: 472
                                                                                                       TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.1%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: artificial sequence
     NUMBER OF SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sun, Bill
APPLICANT: Sun, Cecily R
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: For fusion proteins of human granulocyte colony-stimulaing factor TITLE OF INVENTION: increased biological activities
FILE REFERENCE: 03SUN2001
CURRENT APPLICATION NUMBER: US/10/800,449
CURRENT APPLICATION NUMBER: US/09/968,362
PRIOR PILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 20
LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure OTHER INFORMATION: B)
                                                                                                                                                                                                                            233 APEFAGGPSVFLFFPPKFKDTLMISRTPEVTCVVDVSQEDPEVQENWYVDGVEVHNAKTK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 APEFAGGPSVELFPFRENDTLMISRTPEVITCVVVDVSQEDPEVQENWYVDGVEVHNAKTK 292
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                                                                                                                                                                                1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                          61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                         Score 570; DB 16; Length 4 Pred. No. 7.4e-47; 0; Mismatches 2; Indels
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| Publication No. US20030049683A1
| GENERAL INPORMATION:
| APPLICANT: Bowdish, Katherine S. APPLICANT: Frederickson, Shana APPLICANT: Renshaw, Mark
| TILLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES FILE REFERENCE: 1087-2
| CURRENT FILING DATE: 2001-12-05
| PRIOR FILING DATE: 2001-12-05
| PRIOR FILING DATE: 2001-12-05
| PRIOR FILING DATE: 2001-12-05
| PRIOR FILING DATE: 2001-05-04
| PRIOR FILING DATE: 2001-05-04
| PRIOR FILING DATE: 2001-05-04
| PRIOR FILING DATE: 2001-05-29
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US-10-800-449-20
Sequence 20, Application US/10800449
Sequence 20, Application No. US20040265973A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Cecily R
APPLICANT: Sun, Cecily R
                                                                      97.8%;
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ORGANISM: Artificial Sequence
                                                                      Query Match
Best Local Similarity 98.2
Matches 108; Conservative
OTHER INFORMATION: B)
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US-10-800-497-20
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US-10-006-593-67
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Sequence 24, "Application US/11018102; Publication No. US20050136061A1; GENERAL INFORMATION:
    APPLICANT: CENTOCOT. Inc.
    TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES; PILE REFERENCE: CENSO45 USA NP; CURRENT APPLICATION NUMBER: US/11/018,102; CURRENT FILING DATE: 2004-12-21; NUMBER OF SEQ ID NOS: 28; SOFTWARE: Patentin version 3.3; SEQ ID NOS: 28; SEQ ID NOS: 28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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           PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Pred. No. 4.6e-47;
0; Mismatches 3; Indels
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US-11-018-102-24
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Best Local Similarity
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                                                                                                                       RESULT 15
US-11-018-102-24
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APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: GB0324368.0
PRIOR PILING DATE: 2003-10-17
PRIOR PILING DATE: 2003-10-17
SOFTWARE: Patentin version 3.3
SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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APPLICANT: Renshaw, Mark
APPLICANT: Orencia, Cecilia
TITLE REFERENCE: 1087-2 CIP III
CURRENT APPLICATION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2 CIP III
CURRENT APPLICATION NUMBER: US/10/737, 290
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: US 10/307, 724
PRIOR FILING DATE: 2003-6-02
PRIOR FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
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PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-05
NUMBER OF SOC ID NOS: 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Humanized antibody heavy chain US-10-737-290-67
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Pred. No. 4.6e-47;
0; Mismatches 3;
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Best Local Similarity 97.3%;
Matches 107; Conservative
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ORGANISM: Homo sapiens
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Aay54997 N
Aar27680 N
Aar41684 U
Adh75385 N
Adj52132 O
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Maximum Match 100%
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length: 110
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                                                                   OM protein
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Maximum DB
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                                                                                                      Run
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.52 Bovine Ig	Adr59152	ADR59152	œ	46	33.6	196	42
7	Adr5914	ADR59147	œ	46	33.6	196	44
.44 Optimum I	Adr59144	ADR59144	ω	20	34.1	199	43
	Aar33316	AAR33316	7	110	34.6	201.5	42
40 Human col	Aab53640	AAB53640	m	96	34.8	203	41
	Adr59148	ADR59148	æ	46	35.3	206	40
.45 Pig IgG2a	Adr59145	ADR59145	œ	46	35.3	206	39
	Adr59141	ADR59141	æ	46	35.3	206	38
-	Adr59140	ADR59140	œ	46	35.3	206	37
142 Rhesus mo	Adr59142	ADR59142	۵	46	38.6	225	36
43 Rhesus mo	Adr59143	ADR59143	œ	46	38.9	227	35
	Aar33315	AAR33315	~	110	39.9	232.5	34
138 Human IgG	Adr59138	ADR59138	æ	46	40.0	233	33
	Adr59139	ADR59139	8	46	40.0	233	32
	Aap83205	AAP83205	٦	56	46.5	271	31
306 Sequence	Aap83206	AAP83206	Н	26	46.5	271	30
202 Sequence	Aap83202	AAP83202	Н	26	47.3	276	53
	Aap83203	AAP83203	٦		47.5	277	28
201 Sequence	Aap83201	AAP83201	٦		47.5	277	27
204 Sequence	Aap83204	AAP83204	-	26	48.4	282	56

ALIGNMENTS

Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AlDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell. Undefined ORF2 encoded by plasmid pAH4808 AAR41717 standard; protein; 110 AA 92WO-US010206 91US-00800458 (revised)
(first entry) (ALKE-) ALKERMES INC WO9310819-A1. 26-NOV-1991; 24-NOV-1992; 25-MAR-2003 20-OCT-1993 10-JUN-1993 Synthetic. AAR41717; RESULT 1 AAR41717

Friden PM;

WPI; 1993-196742/24. N-PSDB; AAQ43848 Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders.

Disclosure, Fig 19J; 151pp; English.

The sequences given in AAR41715-18 are encoded by the expression vector pAH4808. This vector represents the cloning of the human gamma isotype, gamma-4, with the variable region of the murine monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding (FHL, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones were isolated.

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128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent enerological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                            1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell activating and immunosuppressive activity, and is used to treat transplant patients to prevent rejection. The antibody can be engineered to contain a human Fc region. By transferring the binding specificity into a human framework, the immunogenicity is reduced without affecting the immunosuppressive activity. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanised OKT3 antibody with mutated Fc receptor binding region -useful as immunosuppressant to reduce transplant rejection, lacks the T-cell activating side effects of wild type antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) has potent T-
                                                                                                                                                                                                                                     1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OKT3; monoclonal antibody; antibody engineering; immunosuppressive; humanized antibody.
                                                                                                                                                                                                                                                                                                       PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                           PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                      Length 110;
                                                                                                                                                                                                       3; Indels
                                                                                                                                                                    Score 565; DB 2;
Pred. No. 4.9e-49;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 82-87; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jolliffe L;
                                                                                                                                                                                                                                                                                                                                                                                                                           AAR67438 standard; protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OKT3 monoclonal antibody fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US006198.
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                                                                                                                                                                      96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                 Query Match
Best Local Similarity 97.3
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bluestone JA, Zivin RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ARCH-) ARCH DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-022721/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAQ75356
                                                                                                                                     Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9428027-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1993;
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08-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR67438;
                                                                                                                                                                                                                                                                                                         61
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This sequence represents the mutated CH2 molecule Gideltaac, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement capable of binding domain capable of binding a target molecule; and comprises: (a) a binding domain capable of binding a target molecule; and comprises: (b) an effector domain that is homologous to all or part of a constant companin of a human immunoglobulin G (IgG) heavy chain. The binding constant companing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule is useful for the treatment of graft-vs-chost disease, organ transplant rejection, bone-marrow transplant rejection, autoimmune thrombocytopaenia and arthritis), alloimmune thrombocytopaenia and arthritis), alloimmunity (e.g. vascullitis, autoimmunity (e.g. crohn's, HDN cartell/neonatal alloimmune thrombocytopaenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN cartery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FcgammaR and desirable IgG properties have been retained. The polypeptides do not contain non-
                                                                                                                                                                                                                                                                                                                                                                                                                    Binding molecule, CH2 sequence; complement dependent lysis; FcgammaRIIb; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-vs-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; autoimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopaenia; Goodpastures disease; therapy;
61
                         1 PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin
2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                 REEQFNSTYRVVSVLTVIHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                     62 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sickle cell anaemia; coronary artery occlusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williamson LM;
                                                                                                                                                                                                                                              Ä
                                                                                                                                                                                                                                           AAY54998 standard; protein; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 17; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                             sequence Gldeltaac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-GB001441
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Armour KL, Clark MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-039075/03.
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                                                                                                                                                                                                                                                                                                                                   17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                               Mutated CH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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Gaps

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96.2%; Score 561; DB 2; Length 109; 97.2%; Pred. No. 1.2e-48; ive 0; Mismatches 3; Indels

Conservative

Best Local Similarity Matches 106; Conserv

Query Match

Sequence 109 AA;

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human amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent with being able to cross the human placenta through interaction with FCRn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the mutated CH2 molecule Gldeltaab, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant domain of a human immunoglobulin G (196) heavy chain. The binding molecule is used to bind a target molecule (especially FcgammaRIIb causing inhibition of B call activation, mast cell degrammaRIID phagocytosis). The binding molecule can be used to prevent or inhibit the binding of a second binding molecule, e.g. an antibody, to the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-va-host disease; organ transplant rejection; alloimemune disease; asthma; alloimemune disorder; autoimmune disease; asthma; allergy; autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopaenia; doodpastures disease; therapy;
                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                    1 APPVAGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties.
                                                                                                                                                                                                              1 APPVAGGPSVPLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                             PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                            ;
0
                                                                                                                                    Length 110;
                                                                                                                                  Score 560; DB 3; Length 11
Pred. No. 1.6e-48;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sickle cell anaemia; coronary artery occlusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williamson LM;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY54996 standard; protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Fig 17; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutated CH2 sequence Gldeltaab.
                                                                                                                                 96.1%;
96.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-GB001441,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                      Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark MR,
                                                         (neonatal Fc receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-039075/03.
                                                                                                                                                      Local Similarity
                                                                                                 Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9958572-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY54996;
                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
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molecule. The binding molecule is useful for the treatment of graft-vs-host disease, organ transplant rejection, bone-marrow transplant rejection, autoimmunity (e.g. vascullitis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia and arthritis), alloimmunity (e.g. or fortal/neonatal alloimmune thrombocytopaenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and coronary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FcgammaR and desirable IgG properties have been retained. The polypeptides do not contain non-human amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent with being able to cross the human placenta through interaction with FCRn
                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AlDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAR41707-09 are encoded by the expression vector pAH4625. This vector represents the cloning of the human gamma isotype, gamma-2, with the variable region of the murine monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PREBQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                           DB 3; Length 109;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                         95.1%; Score 554.5; DB 3; 96.4%; Pred. No. 5.5e-48; ive 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Undefined ORF2 encoded by plasmid pAH4625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 17J; 151pp; English.
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 96.4
Matches 106; Conservative
                                                                                                                                                                                                                                                 (neonatal Fc receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
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                                                                                                                                                                                                                                                                                        Sequence 109 AA;
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20-OCT-1993
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heavy chain (VH) is derived from a murine source and the sequences encoding CH1, CH2 and CH13 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ4845), was transfected into SP2/0 cells and clones were isolated.

128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical neurological disorders egg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
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  128.1. This plasmid encodes a chimeric monoclonal antibody in which the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVA-GPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.1%; Score 542.5; DB 2; Length 109; 93.6%; Pred. No. 8.9e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 93.6
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                      Sequence 109 AA;
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AAY54997 standard; protein; 109 AA. Mutated CH2 sequence G2deltaa. (first entry) 17-FEB-2000 AAY54997; RESULT

Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis, vasculitis; Crohn's disease; graft-va-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; sickle cell anaemia; coronary artery occlusion.

Synthetic.

WO9958572-A1

99WO-GB001441 07-MAY-1999;

98GB-00009951 08-MAY-1998; Williamson LM; Clark MR, Armour KL,

(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

WPI; 2000-039075/03.

Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties.

Claim 12; Fig 17; 81pp; English.

Humanised antibodies having modified allotypic determinant - useful for matching allotypes in therapy with decreased likelihood of causing undesirable immune responses.

Disclosure; Fig 4c; 57pp; English.

This sequence represents the mutated CH2 molecule G2deltaa, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement

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dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant cannot be a human immunoglobulin G (IgG) heavy chain. The binding causing inhibition of B cell activation, mast cell degranulation or pagocytosis). The binding molecule can be used to prevent or inhibit the binding inhibition of B cell activation, mast cell degranulation or causing inhibition of B cell activation, bused to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule is useful for the treatment of graft-vs-condition, autoimmune transplant rejection, bone-marrow transplant concertion, autoimmune thrombocytopaenia and arthritis, alloimmunity (e.g. vasculitis, autoimmune hambocytopaenia and arthritis), alloimmunity (e.g. catoingunity collusion). The binding molecules on the catoin correct inflammatory diseases (e.g. Crohn's, HDN chronatal alloimmune thrombocytopaenia and arthritis conversed on the transplant correct inflammatory diseases (e.g. Crohn's, HDN correct activate complement or trigger cytotoxic activities through FcgammaR and desirable corronary artery occlusion). The binding molecules do not contain nonhuman amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent conversed to the polypeptide of the corrors the human placenta through interaction with FCRn corrors the human placenta through interaction with FCRn corrors to the human placenta through interaction with FCRn corrors to the human placenta through interaction with FCRn corrors the mannon acids through placenta through interaction with FCRn corrors to the human placenta through interaction with FCRn corrors the human placenta through interaction with FCRn corrors the human placenta through interaction with FCRn corrors are the transparent corrections the human placenta through interaction the polyperice corrors the human p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 PREEQFINITERVISVLTVVHQDMLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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93.1%; Score 542.5; DB 3;
Best Local Similarity 94.5%; Pred. No. 8.9e-47;
Matches 104; Conservative 2; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR27680 standard; protein; 110 AA
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Best Local Similarity
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10-MAR-1993
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AAR27680
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Transcription of the VH gene is from the VH promoter of the murine 27.44 gene. The vector also includes a heavy chain immunoglobulin enhancer and the human gammal constant region (CH). The VH region of 128.1 was isolated by polymerase chain reaction and cloned into plasmid pAH4274.

This was achieved by digesting the plasmid and the product with EcoRV and Nhel. The VH gene was inserted in-frame with the human gammal CH region CH at the 3' end of the VH-J region by means of a Nhel site. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin
In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17. The inventor's propose eliminating these allotypes by amino acid changes to agree with the sequences of IgG2, IgG3 and IgG4. None of the allotype sites (1, 2 and 17) are located within the CH2 domain. New "isoallotypes" should be suitable for therapeutic use in all patients. See AAR27678-R27681. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                      1 APELLGGPSVFLFPPKPKDTLMISRIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light; chain; variable; constant; region; anti-human; transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease.
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological disorders.
                                                                                                                                                                                                                                                                                                                          PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                         Length 110;
                                                                                                                                                                       Score 541; DB 2; Length 11
Pred. No. 1.3e-46;
4; Mismatches 5; Indels
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                                                                                                                                                                     92.8%; sal Similarity 91.8%; 101; Conservative
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N-PSDB; AAQ43844.
                                                                                                                                   Sequence 110 AA;
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Best Local 8
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                                                                                                                                                                                                                                         1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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receptor on brain capillary endothelial cells. This antibody may be use in a conjugate in which it is linked to a neuro- pharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                     1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC; autoimmune disease; human; IgG; immunoglobulin.
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                                                                                                                                                      Length 110;
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                                                                                                                                                   92.8%; Score 541; DB 2; I 91.8%; Pred. No. 1.3e-46; iive 4; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                             ADH75385 standard; protein; 110 AA
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91.8%;
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Best Local Similarity 91.8
Matches 101; Conservative
                                                                                                                                                                    Best Local Similarity 91.6
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human IgG1 CH2 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allan B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WATK/) WATKINS J D. (ALLA/) ALLAN B.
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                                                                                                                     Sequence 110 AA;
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                                                                                                                                                    Query Match
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obstetric, haematologic, immunological, allergic,

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CHI deleted mimetibody; osteopathic; cardiovascular-Gen;

dermatological-Gen; andiory; endocrine-Gen; gastrointestinal-Gen;

gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;

antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;

mitallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;

mobhthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;

my TNF; cytostnne; bone disorder; joint disorder; cardiovascular disorder;

mose disorder; oral disorder; dermatological disorder; metabolic disorder;

mose disorder; throat disorder; dematological disorder; hepatic disorder;

mose disorder; haematologic disorder; immunological disorder;

allergic disorder; heematologic disorder; musculoskeletal disorder;

allergic disorder; pediatric disorder; nutritional disorder;

pobthalmologic disorder; pediatric disorder; psychiatric disorder;

renal disorder; pediatric disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them). Compositions, methods and uses. The invention may be useful for the development of compounds with an osteopathic.

Cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen, gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic, immunomodulator, antialleragic, muscular-Gen, cytostatic, nephrotropic or antinflammatory, neuroleptic, ophthalmological, nephrotropic or respiratory-Gen activity acting as a tumour necrosis factor (TNF)-

cmodulator or cytokine-agonist. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression cardiovascular, dental or roral, dermatological, ear, nose or throat, cardiovascular, dental or roral, dermatological, ear, nose or throat, cendocrine, metabolic, gastrointestinal, gynaecological, hepatic,
                                         9
1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                        New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic and nutritional disorders.
                                                                                 PREEQFINSTYRUVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                           Ghrayeb J, Scallon BJ, Nesspor TC;
                                                                                                                                                                                                                                                                                                                                                            CH1 deleted mimetibody-related CH2 peptide SegID1124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; SEQ ID NO 1124; 123pp; English.
                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                   ADJ52132 standard; protein; 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUN-2002; 2002US-0392431P.
19-SEP-2002; 2002US-0412144P.
                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-082872/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kutoloski KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                  06-MAY-2004
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                                                                                                                                                                                                                                                                         ADJ52132;
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                                                                                                                                                                                                           ADJ52132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritc; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; immunoglobulin heavy chain; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antigon condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid archritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide that is fused to the M3 constant region polypeptide that is fused to the CH2 constant region polypeptide comprises a wild-type human IgG1 immunoglobulin hinge region polypeptide, a mateated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues;
                                                                                                                                                                                                                                                   89
                                                                                                                                                                                                                                                                                            9
               musculoskeletal, oncological, neurological, nutritional, ophthalmologic, peddiatric, renal or pulmonary disorders. The present sequence is that of a CH2 peptide which may be used during the creation of a memetibody peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                           1 SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKFREEQFNS
                                                                                                                                                                                                                                                   9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binding domain-immunoglobulin fusion protein-associated protein #107.
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                                                                                                                                                                  Length 102
                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                   69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                             61 TYRVVSVLTVLHODWLNGKEYKCKVSNKGLPSSIEKTISKAK 102
                                                                                                                                                                92.3%; Score 538; DB 8; I
100.0%; Pred. No. 2.3e-46;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                    Best Local Similarity 100.0
Matches 102; Conservative
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                                                                                                                         Sequence 102 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD25659;
                                                                                                                                                                  Query Match
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sequences on may be

autoimmune diseases,

Modified immunoglobulins useful in the treatment of autoimmune diseases comprises at least one amino acid modification relative to a wild-type

immunoglobulin constant domain.

Dall'acqua W, Johnson LS,

WPI; 2002-666925/71

(MEDI-) MEDIMMUNE INC

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where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from cysteine residues and a muteted human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residues and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein, a recombinant expression construct path and a remain polypeptide is capable of specifically binding to an antigen. Also included are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a plarmaceutical composition comprising the binding domain-immunoglobulin fusion protein is useful for treating a parapected of having a malignant condition or a B-cell disorder. Chaving or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein sequence is a binding domain-immunoglobulin fusion protein sequence is a binding domain-immunoglobulin fusion protein sequence is a binding domain-immunoglobulin fusion protein sequence is a binding domain manusing aravis, Grave's disease. The present sequence is a binding domain and saviable in electronic format directly from USPTO and and is also available in electronic format directly from USPTO and and is also available in electronic format directly from USPTO and and is also available in electronic format directly electronic format or therefore none of the sequences and be explicitly by any par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FELLGGPSVFLFPPRKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia; vaccination; hypogammaglobulinaemia; autoimmuno disease; antibacterial; immunosuppressive; lymphoid malignancy; respiratory syncytial virus; anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunoglobulin G1 (IgG1) Fc region second constant (CH2) domain.
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nes 100; Conservative
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The invention relates to a modified immunoglobulin (IgG1) which comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising a variant of a parent polypeptide having least a portion of a Fe region, useful in treating e.g., autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fc region; antibody-dependent cell-mediated cytotoxicity; ADCC; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109
                                                                                                                                                                                                                                                                                                                                                                       Score 536; DB 5; Length 109;
Pred. No. 4e-46;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, SEQ ID NO 53; 62pp; English.
                                                                                                                                                             Disclosure; Page 138; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH75415 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                       91.9%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91.7'
Matches, 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CH2 region K290S variant.
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                                                                                                                                                                                                                                                                                                                                           Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (WATK/) WATKINS
(ALLA/) ALLAN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004002587-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
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12-DEC-2001; 2001WO-US048432. 12-DEC-2000; 2000US-0254884P. 09-MAY-2001; 2001US-0289760P.

WO200260919-A2

08-AUG-2002.

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Gaps

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Indels

Length 110;

Score 535; DB 8; Len Pred. No. 5.1e-46;

91.8%; 90.9%;

Query Match Best Local Similarity 90.9 Matches 100; Conservative

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Pred. No. 5.1e 4; Mismatches

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APELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110

61 61 ADH75413 standard; protein; 110 AA

RESULT 15

(first entry)

22-APR-2004

ADH75413;

CH2 region D280H variant.

autoimmune disease

US2004002587-A1 Unidentified.

01-JAN-2004

1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK

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                        parent polypeptide having at least a portion of a Fc region. The variant mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells more effectively than the parent polypeptide and comprises at least one amino acid modification at position 280 in the Fc region. The composition is useful in treating diseases e.g., autoimmune diseases. The present sequence represents a CH2 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  having
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                                                                                                                                                                                                                             APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTS
                                                                                                                                                                                    Gaps
             invention relates to a new composition comprises a variant of a
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                                                                                                                                                                                                                                                                                    PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                                                                                                                                       Score 536; DB 8; Length 110;
Pred. No. 4.1e-46;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immune response; immunoglobulin; Ig; CH2 region; human.
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                                                                                                                                                         91.9%;
90.9%;
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14-MAR-2003; 2003WO-US007995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang L, Smith D,
                                                                                                                                                                    Best Local Similarity 90.9
Matches 100; Conservative
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                                                                                                                               Sequence 110 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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region; antibody-dependent cell-mediated cytotoxicity; ADCC;

20-FEB-2003; 2003US-00370749 20-FEB-2002; 2002US-0358161P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APELLGGPSVFLFPPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVHGVEVHNAKTK
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Pred. No. 6.5e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 51; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.6%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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The present invention relates to a method for generating an immune response to an antigen in a patient. The method comprises administering to the patient an immunoglobulin (Ig) or its portion where the Ig has at least one peptide epitope of the antigen attached to the Ig or its portion and administering the immunoglobulin or its portion in conjunction with a RNA segment. A recombinant human Ig molecule capable of binding to an RC gamma receptor (FogammaR) of an antigen presenting cell (APC) was used to illustrate the invention. The recombinant human Ig molecule comprises a CH3 region (ADL90102), a CH2 region (ADL90103), a hinge region (ADL90104) and a flanking peptide (ADL90105).

Sequence 110 AA;

Disclosure; Page 11; 154pp; English.

New composition comprising a variant of a parent polypeptide having at least a portion of a Fe region, useful in treating e.g., autoimmune

Allan B;

Watkins JD,

WPI; 2004-070755/07.

(WATK/) WATKINS J D. (ALLA/) ALLAN B.

Search completed: November 17, 2005, 07:47:01 Job time : 90.9087 secs

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; Search time 16.5753 Seconds (without alignments) 638.529 Million cell updates/sec
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                              2005, 07:37:49
                                                                                    OM protein - protein search, using sw model
                                                                                                                              November 17,
                                                                                                                              Run on:
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1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110 US-09-674-857-12 583 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

44790

length: 0 length: 110 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* 79:* PIR. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

gamma-2b chain Description A30503 I68730 I68726 K3HU S43147 ü Query Match Length DB 133 128.5 128.5 128.5 127.5 120.5 120.5 1118 Score Result No.

Ig lambda-2 chain	lambda-chain C-reg	Ig kappa-B9 chain	Ig kappa chain C r	Ig lambda-3 chain	_	σ	Ig kappa chain C r	Ig light chain C r	Ig light chain C r	Ig lambda2-like ch	Ig gamma-3 chain C	_	Ig lambda-2 chain	Ig lambda-2 chain	IgE chain C2 regio
B27390	146731	K9RB	KIRTB	L3MS	S22762	S26652	KIRTA	C34509	D34509	157802	A24629	PL0186	L2MS	S22759	168725
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		15.9	15.6		15.4	14.8							13.0	•	

ALIGNMENTS

	RESULT 1	
	A30503	
	Ig gamma-2b chain	Ig gamma-2b chain C region (E5.7A12) - mouse (fragment)
	C;Species: Mus mu	sculus (house mouse)
	C; Date: 31-Mar-19	C;Date: 31-Mar-1989 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
	C; Accession: A30503	
	R, Gilmore, G.L.;	R;Gilmore, G.L.; Bard, J.A.; Birshtein, B.K.
	J. Immunol. 141,	1754-1761, 1988
	A; Title: DNA rear	A, Title: DNA rearrangements affecting both variable and constant regions of 1g H chain g
_	A; Reference numbe	c: A30503; MUID:88315788; PMID:2842402
	A; Accession: A30503)3
	A; Molecule type: mRNA	nrna
	A;Residues: 1-88 <gil></gil>	:GIL>
	A; Cross-references: GB: M21925	s: GB:M21925
	A; Experimental so	A; Experimental source: myeloma cell line MPC11
	A, Note: the autho	A;Note: the authors translated the codon GAG for residue 41 as Ser
	C, Genetics:	
	A; Introns: 46/3	
	C; Superfamily: im	C; Superfamily: immunoglobulin C region; immunoglobulin homology
	C; Keywords: immunoglobulin	globulin
	F;1-70/Domain: im	F;1-70/Domain: immunoglobulin homology <imm></imm>
	Ouery Match	47.7%; Score 278; DB 2; Length 88;
	Best Local Simi Matches 48;	Best Local Similarity 63.2%; Pred. No. 6.6e-21; Matches 48; Conservative 15; Mismatches 13; Indels 0; Gaps 0;
		FEVITCHANDUSOED PEVOPENWYVIDGUEVIHNA KTIK DREFORMSTIV RAVSVI, TVI, HODW 83
	Db 1 SLT	SLTPKVTCVVVDVSEDDPDVQLSWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDW 60
	Qy 84 LNG	84 INGKEYKCKVSNKGLP 99
	Db 61 MSG	61 MSGKEFKCKVNNKDLP 76
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Ige chain 3 regions chain (3 regions chain (2) regions chain (2) regions chain (2) gupsilon chain (3) ghapda -5 chain (3) ghapda -5 chain (3) ghapda -2 chain (3) ghapda -1 chain (3) ghapda -1 chain (3) ghapda (3) ghapda (3) ghapda (3) ghapda (3) ghapda (3) ghapda (3) ghapda (3) ghapda (3) ghapda (3) ghapda (4) ghap 826653 826653 826653 830554 830554 832760 822760 8333275 83459 83459 83459 832654 8326 220.... 220... 220... 220... 220... 220... 220... 220... 220... 220.... 220... 220... 220... 220... 220... 220... 220... 220... 220... 220... 220... 220... 220... 220... 220... 220... 220... 220... 105.5 105.5 100 99.5 99.5 99.5 109.5 109.5 108.5

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8 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV--EVHNAKTKPREEQ
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IGB Chain C3 region - mouse (fragment)

IGB Chain C3 region - mouse (fragment)

IGB Chain C3 region - mouse (fragment)

C, Species: Mus musculus (house mouse)

C, Accession: IGB726

R, Shinkal, Y.; Makauchi, H.; Hunjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A; Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid is A; Reference number: IS443; MulD:88152907; PMID:3346043

A; Reference number: IS6726

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Residues: DNA

A; Residues: 1-107 cRES>

A; Cross-references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460

C; Superfamily: immunoglobulin C region; immunoglobulin homology

F; 22-90/Domain: immunoglobulin homology < IMM>
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                   Length 107;
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                                                                                       31; Indels
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       24.0%; Score 140; DB 2; 30.7%; Pred. No. 5.3e-07; iive 22; Mismatches 31;
                                                                                   Conservative
Query Match
Best Local Similarity
Matches 35; Conserv
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A;Residues: 1-106 <SUT>
R;Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
Edl 22, 197-207, 1980
A;Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserving A;Reference number: A90806; MUID:81042304; PMID:6775818
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PEBS Lett. 222, 6-10, 1987

Affitle: Chemical modification of the carboxyl groups of protein substrates enhances thei Afreference number: S05572; MUID:88005152; PMID:3115831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Map position: 2p12-2p12

C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kapp

hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into lan

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;19-89/Domain: immunoglobulin homology <IMM>

F;26-86/Disulfide bonds: #status experimental

F;106/Disulfide bonds: interchain (to heavy chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                           A.Accession: A90806
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-106 cHIE>
A.F. Residues: 1-106 c
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A;Title: Die volstaandige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).
A;Reference number: A91639; MUID:68242259; PMID:5586923
A;Contents: Bence Jones protein Cum
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A,Residues: 1-13,'N',15-106 <TIT>
R;Kohler, H.; Bilmizu, A.; Paul, C.; Putnam, F.W.
Science 169, 56-59, 1970
A;Title: Macroglobulin structure: variable sequence of light and heavy chains.
A;Reference number: A94242; MUID:70201507; PMID:5447531
A;Contents: Waldenstrom's macroglobulin Ou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 1-44,'A',46-56,'Q',58-82,'L',84-106 <HIL>
A;Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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A; Residues: 1-13, N', 15-106 < KOH>
B; Residues: 1-13, N', 15-106 < KOH>
B; Rutth, J.H.; Bowcock, A.M.; Billon, H.A.; Nevo, S.; Cavalli-Sforza, Am. J. Hum. Genet. 48, 613-620, 1991
A; Title: Km typing with PCR: application to population screening.
A; Reference number: A37927; MUID:91150772; PMID:1900145
A; Accession: B37927; MUID:91150772; PMID:1900145
A; Receives: not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 8-106 < KUR>
A; Note: allotype Inv(3)
B; Steiner, V; Chang, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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Best Local Similarity 30.5%; Pred. No. 2.6e-06;
Matches 32; Conservative 26; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:120088; OMIM:147200
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셤 ઠે g

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C;Accession: B26167
R;Parvari, R.; Ziv, B.; Lentner, F.; Tel-Or, S.; Burstein, Y.; Schechter, I.
R;Parvari, R.; Ziv, B.; Lentner, F.; Tel-Or, S.; Burstein, Y.; Schechter, I.
A;Title: Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germl A;Reference number: A26167; MUID:87218480; PMID:3107981
A;Accession: B26167
                                                                                                                                  substitute for human antibodies:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | | : | | | : | : | : | : | : | EXVA--PIITLFPPS-KEELNEATKATLVCLINDFYPS--PVIVDWVIDG-STRSGETTA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
      C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000 C;Accession: $26653  
R;Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L. Hum. Antibodies Hybridomas 1, 23-26, 1990  
A;Title: Potential of primate monoclonal antibodies to substitute for human A;Reference number: $26652; MUID:91355693; PMID:2129418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B26167
Ig lambda chain C region - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun_1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B30554

Ig lambda chain C region - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Species: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 PSVFIFP--PSDEQLKSGTASVVCLLNNFYPREAKVQ--WKVDNALQSGNSQESVTEQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV--EVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQRQSNSQYMASSYLSLSASDWSSHETYTCRVTHNG--TSITKTLKRSE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-103 - RPRs A;Cross-references: UNIPROT:P20763; GB:M33049
A;Cross-references: UNIPROT:P20763; GB:M33049
A;Note: 90-Asp was found in one cDNA clone
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;21-87/Domain: immunoglobulin homology <!MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 103;
                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL;X65287
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: B30554
R; Foley, R.C.; Beh, K.J.
J Immunol. 142, 708-711.
A; Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A; Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A; Reference number: A30554; MUID:89093962; PMID:2492052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.0%; Score 128; DB 2; ilarity 32.3%; Pred. No. 7.7e-06; Conservative 22; Mismatches 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                              F;19-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                          A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-99 <EHR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA; DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 32; Conserv
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B26434

Ig lambda-5 chain C region - mouse
C;Species: May-1988 Hasquence_revision 30-Jun-1991 #text_change 16-Aug-1996
C;Date: 21-May-1988 Hasquence_revision 30-Jun-1991 #text_change 16-Aug-1996
C;Accession: B26434
FSakaquenchi, N.; Melchers, F.
Nature 324, 579-582, 1986
A;Title: Lambda-5, a new light-chain-related locus selectively expressed in pre-B lymphc
                                                                                                                                                                                                                                              RESULT 5
343147
19 upsilon chain - duck (fragment)
C;Species: Anas platyrhynchos (domestic duck)
C;Species: Anas platyrhynchos (domestic duck)
C;Date: 06-Reb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
C;Accession: 843147
R;Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
R;Magor, K.E.; Higgins, Data Library, March 1994
A;Description: Evidence from duck immunoglobulin genes that IgY is the common ancestor A;Accession: S43145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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10 VFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLVTLFLPSLKN-LQPTR-PQLVCL---VSEFYPGTLVVDWKVDGVPVTQGVETTQPSKQ 60
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A;Molecule type: mRNA
A;Redidues: 1-105 <SAK>
A;Cross-references: GB:M30387
A;Cross-references: GB:M30387
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 22.0%; Score 128.5; DB 2; Length 105; Local Similarity 34.3%; Pred. No. 7.3e-06; les 36; Conservative 24; Mismatches 36; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 110;
                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 cMAG>
A;Cross-references: EMBL:X78355; NID:9468612; PID:9468613
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                  FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 FNSTYRVVSVLTVLHODWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
22.6%; Score 132; DB 2; Length 11
Best Local Similarity 30.3%; Pred. No. 3.5e-06;
Matches 30; Conservative 20; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK 108
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$26653
Ig kappa chain C region - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
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A;Note: the sequence was determined from an abnormal differentiated gene A;Note: the MOPC 315 cell line produces two light chains, one normal lambda-2 chain and c pears completely normal line produces two light chains, one normal lambda-2 chain and K;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D Nature 299, 380-382, 1982
A;Title: Somatic variants of murine immunoglobulin lambda light chains.
A;Reference number: A993282; MUID:82220143; PMID:6283385
A;Contents: S43
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A;Accession: 393282
A;Accession: 393282
A;Accession: 393282
A;Rolecule type: DNA
A;Residues: 1-105 < 8D2>
B;Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
A;Contents: myeloma protein MOPC 1048
A;Accession: A)3775; MUID:71107854; PMID:5276767
A;Contents: myeloma protein MOPC 1048
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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EMBO J. 6, 927-932, 1987
A;Title: Somatic point mutations in unrearranged immunoglobulin gene segments encoding
A;Reference number: S22759; MUID:87246527; PMID:3109891
A;Accession: S22760
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C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
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F;27-86/Disulfide bonds: #status predicted
F;104/Disulfide bonds: interchain (to heavy chain) #status predicted
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1981 #sequence_revision 29-Jun-1981 #text_change 09-Jul-2004
C;Accesion: A93922, A33251; A93282; A93775; A0226
C;Accesion: A93922, A33251; A93282; A3775; A0226
R;Selsing, E.; Miller, J.; Wilson, R.; Storb, U.
Proc. Natl. Acad. Sci. U.S.A. 79, 4681-4685, 1982
A;Title: Evolution of mouse immunoglobulin lambda genes.
A;Reference number: A93922; MUD:83014953; PMID:6812053
A;Reference number: A93922; MUD:83014953; PMID:6812053
A;Residues: 1-105 <SEL.
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A;Accession: $00259 with conceptual translation
A;Status: not compared with conceptual translation
A;Molecule type: DNA
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Ig lambda-5 chain C region - western wild mouse
C;Species: Mus spretus (western wild mouse)
C;Species: 31-Dec-1988 #sequence_revision 07-Sep-1990 #text_change 21-Jan-2000
C;Accession: S00259
C;Accession: S00259
R;Mami, F:; Cazenave, P.A.; Kindt, T.J.
EMBO J: 7, 117-122, 1988
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A;Molecule type: DNA
A;Residues: 1-105 <B01>
A;Cross-references: GB:J00582; NID:g197595; PIDN:AAA51636.1; PID:g197598
                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                              DB 2; Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 106;
                                           C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;20-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-106 - MAM>
A; Note: the sequence was translated from the germline gene
C; Superfamily: Immunoglobulin C region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F;21-89/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 TNNKYMVSSYLTLISDQWMPHSRYSCRVTHEG--NTVEKSVSPAE 104
                                                                                                                                                                                                                                                        Query Match 21.9%; Score 127.5; DB 2; Length Best Local Similarity 30.8%; Pred. No. 9.2e-06; Matches 32; Conservative 21; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 35; Conserv
A;Residues: 1-105 <FOL>
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61

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RESULT 11 LIMS

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Gaps

Gaps

4

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8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG-VEVHNAKTKPREEQF
                             A;Accession: B34509
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-102 <SCH>
A;Cross-references: GBMZ9044; NID:g212941; PIDN:AAA49153.1; PID:g212942
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                         Query Match
19.9%; Score 116; DB 2; Length 102;
Best Local Similarity 31.5%; Pred. No. 0.00013;
Matches 29; Conservative 18; Mismatches 41; Indels
A; Reference number: A34509; MUID: 90099382; PMID: 2513577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::|: | | ||: | | |: | | |: : | DNTFSVSSYLTLSASDWNSHELYSCLVKHEAL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGL 98
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ne : 17.5753 secs
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B134509

1g light chain C region 3 - sandbar shark (fragment)

C;Species: Carcharhinus plumbeus (sandbar shark)
C;Species: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 17-Nov-2000
C;Date: 22-Jun-18509
C;Accesslon: B34509
R;Schluter, S.F.; Hohman, V.S.; Edmundson, A.B.; Marchalonis, J.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 9961-9965, 1989
A;Title: Evolution of immunoglobulin light chains: cDNA clones specifying sandbar shark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 E
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A37927
Ig kappa chain C region (allotype Inv(1,2)) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Accession: A37927
A; Murth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
A, Accession: A37927; MUID:91150772; PMID:1900145
A; Reference number: A37927; MUID:91150772; PMID:1900145
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 12-81/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PVAGGPSVFLFPPKPTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE----VHNAK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PVA--PTVLIFPPSPAE--LATGTATIVCV---ANKYFPDVTVTWKVDGTTQTTGIENSR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV--EVHNAKTKPREEQFNS 68
                      F53275

Ig kappa-1 chain C region b95 allotype - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: O2-May-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: F53275
R;Ayadi, H.; Marche, P.N.; Cazenave, P.A.
Immunogenetics 34, 201-207, 1991 immunoglobulin kappa chain genes.
A;Ritle: Evolution of the rabbit immunoglobulin kappa chain genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                A.Accession: F53275
A.Acteuus: preliminary
A.Molecule type: DNA
A.Residues: 1-104 < AYA>
A.Residues: 1-104 < AYA>
A.Note: sequence inconsistent with nucleotide translation
A.Note: sequence extracted from NCB1 backbone (NCBIN:56086, NCBIP:56170)
C.Superfamily: immunoglobulin C region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:19-87/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK 108
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Matches 29; Conserv
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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November 17, 2005, 07:13:34 ; Search time 77.8539 Seconds (without alignments) 723.518 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-674-857-12 583 1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110 Title: Perfect score: Sequence:

Scoring table:

1612378 seqs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

301588 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 110

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		P20763 gallus gall	P20765 mus spretus	P01843 mus musculu		P01840 oryctolagus	Q8tcj5 homo sapien			P01847 oryctolagus	P20766 rattus norv		P01839 oryctolagus		_		œ	P01835 rattus norv	_	P01836 rattus norv	P01844 mus musculu	Q99jc1 mus musculu			P79659 oncorhynchu	_	P80697 homo sapien	Q61bv9 mus musculu	_	Q7xzf9 oryza sativ	Q8fby4 escherichia
SUMMAKIES		ΩI	KAC HUMAN	LAC CHICK	LACS_MUSSP	LAC1_MOUSE	LACS_MOUSE	KAC4_RABIT	Q8TCJS	LAC_HUMAN	KAC6 RABIT	LAC RABIT	LACI RAT	LAC PIG	KACB RABIT	KAC_MOUSE	KAC5_RABIT	LAC2_RAT	KAC9_RABIT	KACB_RAT	LAC3_MOUSE	KACA_RAT	LAC2_MOUSE	Q99JC1	QBKYIO	QGEZIS	P79659	P79660	SNSP HUMAN	Q6LBV9	Q6LBW2	Q7XZF9	Q8FBY4
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di	Query	Match	22.8	22.0	21.0	20.7	20.5	19.6	19.3	18.8	18.2	18.1	17.2	17.1	17.1	17.0	16.1	16.1	15.9	15.6	15.4	14.8	13.0	13.0	12.2	12.2	10.7	10.7	10.6	10.6	10.5	10.5	10.1
		Score	133	128	122.5	120.5	119.5	114	112.5	109.5	106	105.5	100	99.5	99.5	66	94	94	92.5	91	90	98	96	92	71	71	62.5	62.5	62	62	61.5	61	59
	Result	No.		8	е	4	ស	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

Q31158 mus musculu O19471 mus musculu O19472 mus musculu O6974 bos taurus O9quh8 mus musculu Q971t6 sulfolobus Q9jkpl marmota mon O66084 lactococcus P79661 oncorhynchu Q26372 trypanosoma Q31248 peromyscus Q31261 rattus norv Q30837 ovis aries G6ehzl homo sapien
Q31158 O19471 O19472 O6GV14 O9QUH8 ALBZ_SULTO O9JNF1 P79661 P79661 Q31248 Q31248 Q31261 Q30837
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993 993 110 110 100 100 63
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## ALIGNMENTS

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                                                                                        MEDLINE=69234734; PubMed=4893682;
Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. 3. The
complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3560(1969).
The complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                                                                                                                                                TISSUE-Abdominal adipose tissue;
MEDLINE-98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
Olsen K.E., Sletten K., Westermark P.;
"Extended analysis of AL-amyloid protein from abdominal wall subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
Biochem. Biophys. Res. Commun. 245:713-716(1998).
-!- MISCELLANEOUS: The EU sequence has the INV (3) allotypic marker, Ala-45 and Val-83. The ROY sequence has the INV (1,2) allotypic marker, Ala-45 and Leu-83.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1. PROSITE; PS50815; IG_LIKE; 1. PROSITE; PS508190; IG_MHC; 1. BROSITE; PS00290; IG_MHC; 1. 3D-structure; Direct_protein sequencing; Immunoglobulin C region;
                                                                                                                                                                                                                     MEDLINE=70201507; PubMed=5447531;
Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interchain (with a heavy chain). V -> L (in INV(1,2) marker). FTIG=VAR 003897. D -> N (in Ref. 5 and 8). E -> Q (in Ref. 5 and 6).
                                    Oppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
                                                                                                                                                                                                       SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1D5B; X-ray; A/L=1-103.
PDB; 1D5B; X-ray; A/L=1-103.
PDB; 1D5C; X-ray; L=1-103.
PDB; 1HEZ; X-ray; L=1-103.
PDB; 1HKZ; X-ray; L=1-106.
PDB; 1MIM; X-ray; L=1-106.
PDB; 1MIM; X-ray; L=1-106.
PDB; 1MIM; X-ray; L=1-106.
PDB; 1MIM; X-ray; L=1-106.
PDB; 1MIM; X-ray; L=1-106.
PDB; 1MIM; X-ray; L=1-106.
PDB; 1MIM; X-ray; L=1-106.
PDB; 1MIM; X-ray; L=1-106.
PDB; 1MIM; X-ray; L=1-106.
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PDB; 1MIM; X-ray; L=1-106.
PDB; 1MIM; X-ray; L=1-106.
PDB; 1MIM; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; X-ray; 
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-33; 38-41 AND 62-80.
                                                                       SEQUENCE (BENCE-JONES PROTEIN AG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J00241; AAA58989.1; -.
                                                                                                                                                                                                                                                                                                Science 169:56-59(1970).
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86
106
83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B90562; K3HU.
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106
83
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DISULFID
VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                          8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV--EVHNAKTKPREEQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                             5 PSVFIFP--PSDEQLKSGTASVVCLLNNFYPREAKVQ--WKVDNALQSGNSQESVTEQDS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87218480; PubMed=3107981;
Parvari R., Ziv E., Lentner F., Tel-Or S., Burstein Y., Schechter I.;
"Analyses of chicken immunoglobulin light chain cDNA clones indicate a
few germline V lambda genes and allotypes of the C lambda locus.";
EMBO J. 6.97-102(1987).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                  Query Match 22.8%; Score 133; DB 1; Length 106; Best Local Similarity 30.5%; Pred. No. 1.7e-05; Matches 32; Conservative 26; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 FNSTYRVVSVLTVLHQDWLNGKBYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interchain (with heavy chain)
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1, 11609 MW; 51984DIFDD372CEB CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 lambda chain C region.
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InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00047; ig; 1.
PR0SITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
                                                                                                                                                                                          2 PKVA--PTITLFPPS-KEELNEATKATLVČLINDFYPS--PVTVDWVIDG-STRSGETTA 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88196070; PubMed=3129289;
Mami F., Cazenave P.A., Kindt T.J.;
"Conservation of the immunoglobulin C lambda 5 gene in the Mus gene.";
EMBO J. 7.117-122(1988).
                                                                       Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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د
                                                                                                                                                                                                                                                              62 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                   PORQSNSQYMASSYLSLSASDWSSHETYTCRVTHNG--TSITKTLKRSE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.0%; Score 122.5; DB 1; Length 105; 33.3%; Pred. No. 0.00019; tive 23; Mismatches 38; Indels 9
      Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 Interchain (with heavy chain). 11674 MW; AAB417DF68471A17 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
22.0%; Score 128; DB 1; 30.3%; Pred. No. 5.1e-05; ive 24; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003066; Ig_MHC.
Pfan; PF00047; ig; l.
SMART; SM00407; IGcl; l.
PROSITE; PS008200; IG_MKC; l.
Immunoglobulin C region; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-B lambda-5 chain C region.
Mus spretus (Western wild mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 AA
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                                                                33; Conservative
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105 AA;
                                     Similarity
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35; Conserv
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RESULT 4 LAC1_MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Amino acid sequences of two mouse immunoglobulin lambda chains.";
Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
-!- MISCELLANEOUS: The MOPC 315 cell line produces 2 light chains, 1
normal lambda-2 chain and 1 abnormal lambda-1 chain that is
missing a large part of the V region. The C region sequence (shown
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (S43).
MEDLINE=82220143; PubMed=6283385;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A93922; LING.
PDB; JUNH; X-ray; A=1-105.
InterPro; IPR000710; IQ-like.
InterPro; IPR00047; IQ-like.
Pfam; PF00047; IQ: 1.
PROSITE; PS00230; IG_HIKE; 1.
PROSITE; PS00230; IG_MHC; 1.
3D-structure; Direct_protein sequencing; Immunoglobulin C region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Somatic variants of murine immunoglobulin lambda light chains.";
                                                                                                                                                                                                                                                                                                                                      "Dual expression of lambda genes in the MOPC-315 plasmacytoma."; Nature 290:65-67(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interchain (with heavy chain).
ET -> TE (in Ref. 4).
Q -> E (in Ref. 4).
Missing (in Ref. 4).
S -> SS (in Ref. 4).
S -> SS (in Ref. 4).
E -> Q (in Ref. 4).
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (MOPC 315).
MEDLINE=81148806; PubMed=6259534;
BOCHWell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
Gefter M.L., Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     here) appears completely normal.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                        MEDLINE-83014953; PubMed-6812053; Selsing E., Miller J., Wilson R., Storb U.; "Evolution of mouse immunoglobulin lambda genes."; Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Ig lambda-1 chain C region.
Mus musculus (Mouse).
 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE (MYELOMA PROTEIN MOPC 104E).
MEDLINE=71107854; PubMed=5276767;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J00582; AAA51636.1; -. EMBL; J00587; AAB59672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 298:380-382(1982).
STANDARD;
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                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Appella E.;
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                                                                                                                                                                                            8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV-HNAKTKPREEQF 66
                                                                                                                                                                                                              61
                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=87065143; PubMed=3024017;
Sakaguchi N., Melchers F.;
"Lambda 5, a new light-chain-related locus selectively expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                               Dire-B lymphocytes.";
Nature 324:579-582(1986).
-- TISSUE SPECIFICITY: Selectively expressed in pre-B lymphocytes.
-- SIMILARITY: Contains 1 immunoglobulin-like domain.
-- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                            7;
                                                                                                                                                         20.7%; Score 120.5; DB 1; Length 105; 30.1%; Pred. No. 0.0003; ive 21; Mismatches 44; Indels 7.
                                                                                                                                                                                                                               67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109
                                                                                                                                                                                                                                        11575 MW; A89F2B09BCFCA018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:96E29; IGJ-5.
InterPro; IPR007110; IG-like.
InterPro; IPR003597; IG-like.
InterPro; IPR003066; IG-MHC.
SWART; SM00407; IGG-1; 1.
PROSTTE; PS50835; IG_LIKE; 1.
PROSTTE; PS00290; IG-MHC; FALSE NEG.
Immunoglobulin C region; Immunoglobulin domain.
NON_TER
                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
13 ambda-5 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M30387; -; NOT_ANNOTATED_CDS.
HSSP; P01843; 1JNH.
                                                                                                                                                                 Best Local Similarity 30.1%
Matches 31; Conservative
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 Mus musculus (Mouse)
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P20764;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               8 PSVFLFPPKPKDTLMISRIPEVICVVVDVSQEDP-EVQFNWYVDGVEV-HNAKTKPREEQ 65
                                                                                                                                                                                                                                                                                                                                                                             6 PLVTLFLPSLKN-LQPTR-PQLVCL---VSEFYPGTLVVDMKVDGVPVTQGVETTQPSKQ 60
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Chen K.C.S., Kindt T.J., Krause R.M.;
Chen K.C.S., Kindt T.J., Krause R.M.;
Primary structure of the Lohain from a rabbit homogeneous antibody
to streptococcal carbohydrate. II. Sequence determination of peptides
from tryptic and peptic digests.";
J. Biol. Chem. 250:3289-3296(1975).
I- MISCELLANEOUS: This chain was obtained from antibody to the
specific carbohydrate of group C Streptococci and was isolated
from the serum of a single rabbit.
-I. SIMILARITY: Contains I immunoglobulin-like domain.
                                                                                                                                                                                                                                                                Gaps
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"Rabbit immunoglobulin kappa genes: structure of a germline b4
allotype J-C locus and evidence for several b4-related sequences in
the rabbit genome.";
Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
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MEDLINE=82060334; PubMed=6795636;
Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
"Nucleotide sequence of constant and 3' untranslated regions of a kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";
Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-1986 (Rel. 44, Last annotation update)
19 Kappa-b4 chain C region.
10 Vorctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                            .
6
                                                                                                                                                                                      Length 105;
6 100 Ig-like.
27 86
104 104 Interchain (with heavy chain)
105 AA; 11678 MW; 1F210915904A86AS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TNNKYMVSSYLTLISDQWMPHSRTSCRVTHEG--NTVEKSVSPAE 103
                                                                                                                                                                                                                                                            37; Indels
                                                                                                                                                                                   DB 1;
                                                                                                                                                                               Match 20.5%; Score 119.5; DB 1 Local Similarity 33.3%; Pred. No. 0.00037; les 35; Conservative 24; Mismatches 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=83300036; PubMed=6412231;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00047; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Name=IGLC1;
                                                                                        Name=IGLC2;
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                                                                                                                    Name=IGLC3;
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                                                                                                                                                                                                             3 PVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE----VHNAK 58
                                                                                                                                                                                                                                         2 PVA--PTVLIFPPAADQ--VATGTVTIVCV---ANKYFPDVTVTWEVDGTTQTTGIENSK 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Lymph node;
The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH-NAKTKPREEQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSVTLFPPSSEE--LQANKATLVCLISDF--YPGAVTVAWKADSSPVKAGVETTTPSKQS
                                                                                                                                                                                Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                14;
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                                                                                        Interchain (with a heavy chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.3%; Score 112.5; DB 2; Length 106; 28.7%; Pred. No. 0.0019; ive 22; Mismatches 43; Indels 7
                                                                                                                                               ch 19.6%; Score 114; DB 1; Length 103; I Similarity 31.4%; Pred. No. 0.0013; 33; Conservative 20; Mismatches 38; Indels 3
                                                                                                                                                                                                                                                                       59 TKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE 103
                                                                                                                                                                                                                                                                                        TP--QNSADCTYNLSSTLTLTSTQYNSHKEYTCKVT-QGTTSVVQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AL713800; CAD28551.1; -.
HSSP; P01842; LLIL.
                                                                                                    N -> D (in Ref. 3).
SFC5ACC8B60E68DB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
1-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp667J0810 (Fragment).
Name=DKFZp667J0810;
                                                                                                                                                                                                                                                                                                                                                                                 106 AA
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InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00564; C1-set; I.
SWART; SWOA407; IGC1; 1.
PROSITE; PS50835; IG_LIKE; I.
PROSITE; PS00290; IG_MHC; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                             Created)
PROSITE; PS00290; IG_MHC; FALSE_NEG
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26 85 19
103 103 In
103 AA, 11043 MW;
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STANDARD;

LAC HUMAN P01842; P80423;

RESULT 8
LAC HUMAN
ID LAC H
AC P0184

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SEQUENCE (BENCE-JONES PROTEIN SH).
MEDLINE=70166723; PubMed=4909564;
Titani K., Wikler M., Shinoda T., Putnam F.W.;
"The amino acid sequence of a lambda type Bence-Jones protein. 3. The complete amino acid sequence and the location of the disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                        Milstein C., Clegg J.B., Jarvis J.M.; "Immunoglobulin lambda-chains. The complete amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Bence-Jones-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Amino acid sequence of the (lambda) light chain of a human myeloma immunoglobulin (IgG New).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparative studies on the structure of the light chains of human immunoglobulins. IV. Assignment of a subsubgroup."; J. Biochem. 93:421-429(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ponstingl H., Hess M., Hilschmann N.;
"Structural rule of antibodies. Primary structure of a monoclonal
immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones
protein Kern). V. The complete amino acid sequence and its genetic
interpretation.";
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=9525598; PubMed=7737190;
Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri
"Characterization of the two unique human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The three-dimensional structure of the fab' fragment of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE (BENCE-JONES PROTEIN NIG-64).
MEDLINE-83186114; PubMed-6404900;
Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS MEDLINE-69088380; PubMed=4883841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myeloma immunoglobulin at 2.0-A resolution.";
Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=75013804; PubMed=4415202;
Fett J.W., Deutsch H.F.;
Primary structure of the Mcg lambda chain.";
Biochemistry 13:4102-4114(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG)
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MEDLINE=74109253; PubMed=4814727;
Chen B.L., Poljak R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE (BENCE-JONES PROTEIN KERN).
                                                                                                                                                                                                                                                                                                                                                       oridges.";
J. Biol. Chem. 245:2171-2176(1970)
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Biochemistry 13:1295-1302(1974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bence-Jones protein.";
Biochem. J. 110:631-652(1968)
21-JUL-1986 (Rel. 01, Crea 21-JUL-1986 (Rel. 01, Last 25-OCT-2004 (Rel. 45, Last Ig lambda chain C regions.
                                                                                                                                                              Homo sapiens (Human)
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                                                                                                                                                                                                                                         -I. MISCELLANEOUS: The sequence shown is the Kern-/Oz-/Mcg- chain found in proteins SH, X, and NIG-64. The Kern protein has the Kern+ marker, the NEWM protein has the Oz+ marker, the Mcg protein has the Kern+ marker, and the Mcg+ marker.

-I. MISCELLANEOUS: Six tandem lambda-type genes were identified and the 3 most 5, were sequenced. These correspond to the Mcg sequence (lambda-1), the Kern-/Oz- sequence (lambda-2) and the Kern-/Oz+ sequence (lambda-2) and the Kern-/Oz+
                       Panagiotopoulos N.;
                                                                                                                                                                                  MEDLINE-82080680; PubMed-6273747;
Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
"Clustered arrangement of immunoglobulin lambda constant region genes
                                                                            X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF MCG.
MEDLINE=90133913; PubMed=2215285;
Bly K.R., Herron J.N., Harker M., Edmundson A.B.;
"Three-dimensional structure of a light chain dimer crystallized in water. Conformational flexibility of a molecule in two crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1. PR050121; PR051TE; PS50815; IG_LIKE; 1. PR05ITE; PS0290; IG_MHC; 1. Direct protein sequencing; Immunoglobulin C region; Immunoglobulin domain.
        X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
Edmundson A.B., Ely K.R., Abola E.E., Schiffer M., Panagiotor
"Rotational allomeriem and divergent evolution of domains in
immunoglobulin light chains.";
Biochemistry 14:3953-3961(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interchain (with heavy cha
A -> N (in MCG+ marker).
/FTIG=VAR 003898.
S -> T (in MCG+ marker).
/FTIG=VAR 003899.
S -> G (in Kern+ marker).
/FTIG=VAR_003900.
                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, J00253; AAA59107.1; -.
EMBL, 138562; AAB5681.1; ALT INIT.
EMBL, X51754; CAB38569.1; ALT_INIT.
EMBL, X51755; CAA36049.1; -.
EMBL, X51755; CAA36051.1; -.
PIR, A92057; L2HU.
PDB, 1AQK; X-RAY; L=1-105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [g-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0066955; P:immune response;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; GO:0003823; F:antigen binding;
                                                                                                                                           J. Mol. Biol. 210:601-615(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; ZMCG; X-ray; -...PDB; 7FAB; X-ray; L=1-105.
Genew; HGNC:5855; IGLC1.
Genew; HGNC:5856; IGLC2.
Genew; HGNC:5856; IGLC2.
                                                                                                                                                                                                                     in man.";
Nature 294:536-540(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H-InvDB; HIX0016285; -. MIM; 147220; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
104
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                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                         forms
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PDB;
PDB;
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"A genomic gene encoding the b5 rabbit immunoglobulin kappa constant
region: implications for latent alloxype phenomenon.";
Proc. Natl. Acad. Sci. U.S.A. 81:1789-1793 (1984).

-!- MISCELLANEOUS: The cDNA from which this sequence was derived
contains a terminator codon within the V-region coding region. The
origin of this codon and of the differences between this and other
sequenced b5 C regions are unclear. The cDNA clone was made using
mRNA from trypanosome infected b5-homozygous rabbits.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 PSVFLEPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH-NAKTKPREEQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 PSVTLFPPSSEE--LQANKATLVCLISDF--YPGAVTVAWKADSSPVKAGVETTTPSKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=84041515; PubMed=6314281; Bernstein K.E., Skurla R.M. Jr., Mage R.G.; Bernstein K.E., Skurla R.M. Jr., Mage R.G.; "The sequences of rabbit kappa light chains of b4 and b5 allotypes differ more in their constant regions than in their 3' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11236 MW; DCD9C7C201C13CC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T -> K (in MCG+ marker).
/FTId=VAR_003901.
R -> K (in OZ+ marker).
/FTId=VAR_003902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 18.8%; Score 109.5; DB 1; Best Local Similarity 27.7%; Pred. No. 0.0037; Matches 28; Conservative 23; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-0CT-1986 (Rel. 02, Created)
23-0CT-1986 (Rel. 02, Last sequence update)
23-0T-2006 (Rel. 46, Last annotation update)
1G kappa chain b5 variant C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (CLONE PKB5-F2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                             82
                                                                                                                       105 AA;
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SEQUENCE FROM N.A.
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                                                             82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAC6_RABIT
P03984;
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SEQUENCE
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                                                                                8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEV-HNAKTKPREEQF 66
                                                                                                                          PSVILFPPSSEE--LKDNKATLVCLISDFYPR--TVKVNWKADGNSVTQGVDTTQPSKQS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 PSVPLPPPKPKDTLMISRTPEVT--CVVVVDVSQEDPEVQ-FNWYVDGVEVHNAKTKPREE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 PSVTLFPPSSEEL----KTDKATLVCMVTDFY---PGVMTVVWKADGTPITQGVETTQPF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steen M.L., Hellman L., Pettersson U.; "The immunoglobulin lambda locus in rat consists of two C lambda genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=87305594; PubMed=3114047; DOI=10.1016/0378-1119(87)90250-2;
                          7;
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17.2%; Score 100; DB 1; Length 104;
Best Local Similarity 27.4%; Pred. No. 0.033;
Matches 29; Conservative 22; Mismatches 43; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : |: | : | : | | | : : | | | : : | | | : : | | : | : : | | : | : : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                                                67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                       47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 AA; 11565 MW; CBF71811F4BC878A CRC64;
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InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PPR00407; ig; l..
SMART; SM00407; IGcl; l.
PROSITE; PS00290; IG MHC; l.
Immunoglobulin C region; Immunoglobulin domain.
26.9%; Pred. No. 0.0093;
tive 22; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
10-FEB-1991 (Rel. 17, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
19 lambda-1 chain C_region.
                                                                                                                                                                                                                                                                                                                                                                                                 104 AA
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HSSP; P01843; 1JNH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and a single V lambda gene.";
Gene 55:75-84(1987).
Best Local Similarity 26.99
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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DISULFID
SEQUENCE
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LAC_PIG
ID _ LAC_PIG
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG----VEVHNAKTKPRE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1g lambda chain C region.
1g lambda chain C region.
Cyctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The primary structure of the constant region of Basilea-rabbit immunoglobulin lambda-chains.";
Biochem. J. 197:177-183 (1981).
-i- MISCELLANEOUS: This lambda chain expresses the c7 allotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 105.5; DB 1; Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interchain (with a heavy chain).
A -> VA (in Ref. 2).
7C71850205381751 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.2%; Score 106; DB 1; Length 104; 26.7%; Pred. No. 0.0082; tive 25; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interchain (with heavy chain)
B427513272E8663D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 EQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D--DCTYNLSSTLTLKSDEYNSHDEYTCQVA-QGSGSPVVQSFSR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01842; 1AQK.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR003597; Ig c1.
InterPro; IPR00406; Ig_MHC.
PRam, PPR00407; IG:1, 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; FALSE NEG.
Direct protein sequencing; Immunoglobulin C region; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specificity.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                  HSSP, PO1837; 25C8.
InterPro; IRR007110; Ig-like.
InterPro; IRR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
SWART; SM0407; ig; 1.
PROSITE; PSSO835; IG_LIKE; 1.
PROSITE; PSSO835; IG_MHC; PALSE_NEG.
Immunoglobulin C region; Immunoglobulin domain.
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                 EMBL; X00032; -; NOT ANNOTATED_CDS
EMBL; K01363; AAA31355.1; -.
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Les 28; Conservative
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104
105 AA;
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104
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P01847;
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DISULFID
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RESULT 10 LAC_RABIT

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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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Cell 15:1067-1075(1978)
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106 1
106 AA;
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P01837;
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KAC_MOUSE
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                                                                                                                                                                                                                                                                                                                        Novotny J., Franck F., Margolies M.N., Haber B.;
"Amino acid sequence of normal (microheterogeneous) porcine
immunoglobulin lambda chains";
Blochemistry 16:3765-3772(1977).
-!- MISCELLANEOUS: This chain was obtained from a mixture of normal
                                                                                                                                  Sus scrofa (Pig).
Walaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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105 AA; 11003 MW; 3817AAEBD747C396 CRC64;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003506; Ig_MC.
InterPro; IPR00407; Ig_l.
SMART; SM00407; Igcl; 1.
PROSITE; PS00259; IG_LKE; 1.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain.
                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
22-JUL-2004 (Rel. 44, Last annotation update)
1g lambda chain C region.
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21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
18 kappa-b4 chain C region.
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86
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P01839;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this tatement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-19084137; PubMed=103625; DOI=10.1016/0092-8674(78)90290-8; Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.; "Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the dideoxynucleotide method of RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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"The complete amino acid sequence of a mouse kappa light chain.";
Biochem. J. 128:427-444(1972).
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Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Blochem. J. 126:837-850 (1972).
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11279 MW; AF9B928DDA853849 CRC64;
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PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; FALSE NEG.
Immunoglobulin C_region; Immunoglobulin domain.
NON_TER.
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21-JUL-1986 (Rel. 01, Last sequence update)
25-CTL-2004 (Rel. 45, Last annotation update)
1g kappa chain C region.
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EMBL; V00885; -; NOT_ANNOTATED_CDS.
PIR; A02121; K4RBBS.
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MEDLINE=73053310; PubMed=4638343;
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                                                         SEQUENCE FROM N.A.
MEDLINE-81191915; PubMed=6262318;
Max E.E., Maizel J.V. Jr., Leder P.;
"The nucleotide sequence of a S.5-kilobase DNA segment containing the mouse kappa immunoglobulin J and C region genes.";
J. Biol. Chem. 256:5116-5120(1981).
                                                                                                                                                                                                       MEDLINE-88329081; PubMed-3138116; de Waale P., Fiers W.; de Waale P., Feys W.; van de Voorde A., Molemans F., Fiers W.; Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline
                                                                                                                                   MEDIINE-81198949; Pubmed-6785724;
Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;
"DNA sequence of the constant gene region of the mouse immunoglobulin
MEDLINE-82059477; PubMed=6170937; Hamlyn P.H., Gait M.J., Milatein C.; "Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxynuclectide method of RNA sequencing."; Nucleic Acids Res. 9:4485-4494(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein sequencing; Immunoglobulin C region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interchain (with a heavy chain)
                                                                                                                                                                                                                                                     Bur. J. Biochem. 176:287-295(1988).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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                                                                                                                                                                   kappa chain.";
Nucleic Acids Res. 9:971-981(1981)
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PDB; 1RSK; X-ray; B/E=1-106.
PDB; 1KB5; X-ray; L=1-106.
PDB; 1KCS; X-ray; L=1-106.
PDB; 1KCS; X-ray; L=1-106.
PDB; 1KCV; X-ray; L=1-106.
PDB; 1KCV; X-ray; L=1-106.
PDB; 1CV; X-ray; L=1-106.
PDB; 1ORQ; X-ray; A=1-106.
PDB; 2CS; X-ray; A=1-106.
PDB; 2CS; X-ray; L=1-106.
PDB; 2CS; X-ray; L=1-106.
PDB; 2CS; X-ray; L=1-106.
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InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig_MHC.
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SMART; SM00407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chersi A., Alexander C.B., Mage R.G.; "Partial primary structure of the immunoglobulin light chain constant region of a single rabbit of b5 allotype.";
                                                                                                                                                                                                                                                            6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 4-103.
MEDLINE=82057807; PubMed=6795448; DOI=10.1016/0161-5890(80)90177-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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                                                                                                                                                                                                                Query Match 17.0%; Score 99; DB 1; Length 106; Best Local Similarity 25.2%; Pred. No. 0.042; Matches 26; Conservative 23; Mismatches 48; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK 108
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Direct protein sequencing; Immunoglobulin C region; Immunoglobulin domain.
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P -> S (in Ref. 2).
A -> T (in Ref. 2).
E -> Q (in Ref. 2).
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1g kappa-b5 chain C region.
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11778 MW;
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Biochemistry 22:993-998(1983).
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HSSP, PO1837; IKCU.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR03006; Ig_MHC.
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103 AA;
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Best Local Similarity 29.0%; Pred. No. 0.13; Matches 29; Conservative 19; Mismatches 40; Indels 12; Gaps 5;
                                       64 EQFNSTYRVUSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE 103
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60 D--DCTYNLSSTLTLQKSNYNSHNEYTCQVA-QGAGSVVQ 96
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Search completed: November 17, 2005, 07:52:17 Job time : 77.8539 secs

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LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
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STATE: MA
COUNTRY: USA
ZIP: 02173
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 Sequence 44, Appl Sequence 44, Appl Sequence 4, Appl Sequence 30, Appl Sequence 31, Appl Sequence 21, Appl Sequence 21, Appl Sequence 38, Appl Sequence 38, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl
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1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110
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Copyright (c) 1993 - 2005 Compugen Ltd.
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-09-490-070A-166
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US-08-22-246A-44
US-08-557-050-4
US-08-444-644-30
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US-08-232-246A-31
US-08-232-246A-31
US-08-232-246A-38
US-08-232-239D-60
US-08-232-239D-60
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US-08-802-077-1
US-09-802-077-1
US-08-422-091-10
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 44, Application US/08232246A
Patent No. 6329508
GENERAL INFORMATION:
TEXT TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF SEQUENCES: 46
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                           Gaps
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1.3e-60;
                                                                                                                           3; Indels
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STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPOTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION: 530
                                                                               Score 565; DB 3;
Pred. No. 1.3e-60;
0; Mismatches 3;
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Pred. No. 1.3e
0; Mismatches
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REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-9540
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 07/800,458
FILING DATE: 26.NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                   96.9%;
97.3%;
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Matches 107; Conservative
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amino acid
                                                                            Query Match 96.99
Best Local Similarity 97.3
Matches 107; Conservative
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      protein
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MEDIUM TYPE: Floppy
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; MOLECULE TYPE;
; FRAGMENT TYPE;
US-08-444-644-44
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FRAGMENT TYPE:
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ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-08-232-246A-44
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1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

Gaps

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3; Indels

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1 APEFLGGPSVFLFPPKPXDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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                                                                                                                           61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Patent No. 6491916
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bluestone, Jeffrey A.
APPLICANT: Zivin, Robert A.
APPLICANT: Joiliffe, Linda K.
TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
                                                                                                                                                                                                                                                                                                                                           GENERAL INCORMATION:
APPLICANT: Zivin, Robert A.
APPLICANT: Zivin, Robert A.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Bluescone, Jeffrey A.
TITLE OF INVENTION: Methods and Materials For Modulation
TITLE OF INVENTION: Of the Immuno-suppressive Activity and
TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                          61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 561; DB 2;
Pred. No. 4e-60;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/070,116A
FILING DATE: 01-JUN.1993
CLASSIFICATION: 530
ATTONNEY/AGENT INPORMATION:
NAME: W11son, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: 37,259
REFERENCE/DOCKET NUMBER: 37,259
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America ZIP: 77210
                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08070116A Patent No. 5885573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 96.2%;
Best Local Similarity 97.2%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: P.O. BC
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-070-116A-4
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1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 59
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TRANSFERRIN RECEPTOR SPECIFIC
ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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| Sequence 30, Application US/08232246A
| Patent No. 6329508
| GENERAL INFORMATION:
| APPLICANT Fride No. Fallip M. TITLE OF INVENTION:
| TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DITLE OF INVENTION: AUTIBODY-NEUROPHARMACEUTICAL OR DITLE OF INVENTION: CONJUGATES
| NUMBER OF SEQUENCES: 46
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
| CITY: Lexington | COUNTY: USA |
| COUNTRY:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NDATA:
CAPLICATION NAMBER: US/08/232,246A
         NYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.1%; Score 542.5; DB 3
93.6%; Pred. No. 6.9e-58;
iive 3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALK88-15AAAZ
                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,246
FILING DATE: 07-UL-1994
FILING DATE: 07-UL-1994
APPLICATION NUMBER: 08 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/404,089
FILING DATE: 07-SEP-1990
APPLICATION NUMBER: 08 07/404,089
FILING DATE: 07-SEP-1980
ATTORNEY/AGENT INFORMATION:
         OPERATING SYSTEM: PC-DOS/MS-DOS
SUFTWARE: PATENTIN Release #1.0,
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 amino acids
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Matches 103; Conservative
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internal
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FRAGMENT TYPE:
                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-444-644-30
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         THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL ANTIBODIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 61
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ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
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                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,050
FILING DATE: Concurrently Herewith
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06198
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/070,116
FILING DATE: 01-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two Militia Drive CITY: Lexington COUNTY: Lexington COUNTS: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 96.2%; Score 561; DB 4, Best Local Similarity 97.2%; Pred. No. 4e-60; Matches 106; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:208
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 474-757
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: THE IMMUNO-SUPP
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
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Patent No. 601555
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN REC
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 109 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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STREET: F.c.
TTV: Houston
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US-08-444-644-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-557-050-4
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
PILING DATE: 04-MAY-1994
CLASSIFICATION NUMBER: US/08/232,246A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
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; Sequence 21, Application US/08232246A
; Patent No. 6329508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.8%;
Matches 101; Conservative
     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-444-644-21
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
TOWNER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 PREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٦;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
93.1%; Score 542.5; DB 3; Length 1
Best Local Similarity 93.6%; Pred. No. 6.9e-58;
Matches 103; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02173
COMPUTER: ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
FILING DATE:
                                         FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION WHERE: US O7/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 21, Application US/08444644; Patent No. 6015555; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: (6.17) 861-9540
INFORMATION FOR SEQ ID NO: 30.
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Mili
CITY: Lexington
STATE: MA
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US-08-444-644-21
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Friden, Phillip M.

APPLICANT: Friden, Phillip M.

TITLE OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

TITLE OF INVENTION: CONJUGATES

TITLE OF INVENTION: CONJUGATES

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 541; DB 3;
Pred. No. 1.1e-57;
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATOOMEZ/AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: 34,480
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 861-6240
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TOPOLOGY: linear
MOLECULE TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK
TELECOMMINICATION:
TELEPHONE: (617) 861-6240
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67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                         61 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Matches 99; Conservative
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internal
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FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02173
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COUNTRY:
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                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                         Score 541; DB 3; Length 11 Pred. No. 1.1e-57; 4; Mismatches 5; Indels
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Pred. No. 8.6e-56;
3; Mismatches 3; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 60, Application US/08232539D
Fatent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: 19E Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P0718P3
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APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: POT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.1%;
94.2%;
                                                                                                                                                                                                       Query Match
Best Local Similarity 91.8%;
Matches 101; Conservative
                                                         LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 105 amino acids
Amino Acid
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Best Local Similarity 94.2
Matches 98; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                   MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-232-539D-60
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
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                                                                                       Phillip M.
TRANSFERIN RECEPTOR SPECIFIC
TRANSFORY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.1%; Score 525; DB 3; Length 110; 90.0%; Pred. No. 9.2e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
Sequence 318, Application US/08444644

Patent No. 601555
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIA-
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMUNICATION INFORMATION:
TELEPANE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSOEDPEVOFNWYVDGVEVHNAKTK 60
                                                                                            Phillip M.
TRANSFERRIN RECEPTOR SPECIFIC
ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.1%; Score 525; DB 3; Length 110; 90.0%; Pred. No. 9.2e-56; Live 4; Mismatches 7; Indels
Sequence 38, Application US/08232246A

Patent No. 632950B

GENERAL INFORMATION:

TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIA

TITLE OF INVENTION: CONJUGATES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSE: ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION S30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/05077
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US/08/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US/04/089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US/07/404,089
FILING DATE: 07-SEP-1989
ATPORNEY/AGENT INFORMATION:
APPRICATION NUMBER: 34,480
RECISTRATION NUMBER: 34,480
REPERBNEK-DOCKET NUMBER: 34,480
RECISTRATION NUMBER: 34,480
RECISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/DOCKET NUMBER: 34,480
REFERENCE/OFFERENCE/STICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 90.0
Matches 99; Conservative
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FRAGMENT TYPE: internal
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US-08-569-147-85
                                                                                                                                                                                                                                                                                                                             CITY: Le:
STATE: M.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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Sequence 85, Application US/08569147
Patent No. 6180377
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANISED ANTIBODIES

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Sequence 36, Application US/09281760E

Sequence 36, Application US/09281760E

Patent No. 6734287

GENERAL INFORMATION:

APPLICANT: Lawton, Robert

APPLICANT: Mermer, Brion

TITLE OF INVENTION: Specific Binding Protein for Treating

TITLE OF INVENTION: Canine Allergy

FILE OF INVENTION: Canine Allergy

FILE REPERENCE: 01-1275A

CURRENT APPLICATION NUMBER: US/09/281,760E

CURRENT FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 36

LENGTH: 107
                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,147

FILING DATE: 25-March-1996

CLASSIFICATION: 536

ATTONNEY/AGENT INFORMATION:

NAME: Trujilo, Doreen Yarko

REGISTRATION NUMBER: 35,719

REFERENCE/DOCKET NUMBER: 35,719

REFERENCE/DOCKET NUMBER: 35,719

TELECOMMUNICATION: TROCRATION:

TELECOMMUNICATION: 100: 85:

TELEFAX: (215) 568-3100

INFORMATION POR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

LENGTH: 66 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-569-147-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 66;
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6180377ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc feature
LOCATION: (136)..(136)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.3%; Score 328; DB 3; L. 90.9%; Pred. No. 3.1e-32; ive 3; Mismatches 3;
                                                                                                                       COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.9°
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
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67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.6%; Score 166.5; DB 2; Best Local Similarity 34.3%; Pred. No. 2.1e-12; Matches 35; Conservative 22; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION INDRER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1992-05-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1991-08-14
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-4pr-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           P0718P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08466163B
Patent No. 6329509
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFRENCE/DOCKET NUMBER: P0716
TELEPHONE: 650/22-1489
TELEPHONE: 650/52-9881
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 106 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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US-08-466-163B-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
30.7%; Score 179; DB 4; Length 107;
Best Local Similarity 35.9%; Pred. No. 6.4e-14;
Matches 37; Conservative 22; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109
       LOCATION: (413)..(414)

THER INFORMATION: "n" stands for any nucleic acid
                                                                             NAME/KEY: misc feature
LOCATION: (451)..(451)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (460)..(462)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (500)..(500)
JTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (530)..(530)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (847)..(849)
JTHER INFORMATION: "n" stands for any nucleic acid
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LOCATION: (853)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (1382)..(1382)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature; LOCATION: (1832) ..(1832) ..(1832) ..(1832) ..(1832) ..(1832) ..(1832) ..(1832) ... stands for any nucleic acid US-09-281-760E-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Presea, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: 19E Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-232-539D-54
; Sequence 54, Application US/08232539D
Patent No. 5965709
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
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7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 66
                                                                                                                             1 GVSAYLSRPSPFD-LFIRKSPIITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR 64
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                                                    Gaps
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Length 106;
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Search completed: November 17, 2005, 07:53:56 Job time : 23.6073 secs

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq

557 547.5 545.5 545.5 545.5 545.5 544.5 544.5 542.5

Sequence Sequence

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US-10-959-318-8 US-10-959-318-12 US-10-959-318-15 US-10-959-318-15 US-10-959-318-6 US-10-959-318-6 US-10-959-318-6 US-10-959-318-6 US-10-959-318-2 US-10-959-318-2 US-10-959-318-2 US-10-959-318-2 US-10-959-318-2 US-10-959-318-2 US-10-959-318-2 US-10-959-318-2 US-10-959-318-2 US-10-959-318-2 US-10-959-318-2 US-10-959-318-2 US-10-959-318-2 US-10-059-318-2 US-10-959-318-3 US-10-959-318-3 US-10-959-318-3 US-10-959-318-3 US-10-677-556-278 US-10-677-556-378 US-10-959-318-3

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; Search time 83.1279 Seconds (without alignments) 553.666 Million cell updates/sec
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                                                                                                                                                 1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                              1867879 segs, 418409474 residues
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                                                                         07:47:15
                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                                                           Listing first 45 summaries
                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0% Maximum Match 100%
                                                                       2005,
                                                                                                                         US-09-674-857-12
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                                                                       November 17,
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             Copyright
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Maximum DB seq length: 110
                                                                                                                                                                           BLOSUM62
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Match
                                                                                                                                     Perfect score:
                                                                                                                                                                           Scoring table:
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                                                 •
                                                OM protein
                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                        Database
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No.
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Sequence 22, Appl Sequence 3, Appli Sequence 322, App

ALIGNMENTS

Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence

91.9 91.6

5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245 5245

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                                                                          APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: PT/GB2004/004254
PRIOR APPLICATION NUMBER: GB0324368.0
PRIOR FILING DATE: 2003-10-07
PRIOR FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
SEQ ID NO 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a, ; OTHER INFORMATION: mutations
US-10-959-318-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cch 98.8%; Score 576; DB 18; Length 110; al Similarity 98.2%; Pred. No. 3.9e-48; 108; Conservative 2; Mismatches 0; Indel8
                     ; Sequence 9, Application US/10959318; Publication No. US2005021576BA1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 110
TYPE: PRT
US-10-959-318-9
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Best Local S:
Matches 108
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Sequence 10,
Sequence 24,
Sequence 24,
Sequence 21,
Sequence 21,
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Sequence Sequence Sequence

US-10-959-318-9 US-10-959-318-10 US-11-018-102-25 US-11-018-102-24 US-11-018-102-24 US-10-959-318-13 US-10-959-318-7 US-10-959-318-7 US-10-959-318-11 US-10-959-318-11

576 573 571 565 565 562 562 561 561 560 559 559

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1 APEFLGGPSVFLFPPFKPKDTLMISRTPEVTCVVVDVSQEDPEVOFNWYVDGVEVHNAKTK 60
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Sequence 24, Application US/11018102

Sequence 24, Application US/11018102

Publication No. USCO50136061A1

GENERAL INFORMATION:

APPLICANT: Centcoor, Inc.

TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES

FILE REFERENCE: CENSO4S USA NP

CURRENT APPLICATION NUMBER: US/11/018,102

CURRENT FILING DATE: 2004-12-21

NUMBER OF SEQ ID NOS: 28
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                                                                                                                                              Sequence 4, Application US/10959318
Publication No. US20050215768A1
GENERAL INFORMATION:
APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-030
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: PCT/GB2004/004254
PRIOR FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: GB0324368.0
  61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 565; DB 18;
Pred. No. 4.6e-47;
0; Mismatches 3;
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SOFTWARE: Patentin version 3.3
SEQ ID NO 4
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Best Local Similarity 97.3%;
Matches 107; Conservative (
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TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 110
TYPE: PRT
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US-10-959-318-10
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Publication No. US20050136061A1
GENERAL INFORMATION:
APPLICANT: CENTOCOX, INC.
TITLE OF INVENTION: ANTI-RETROVIRAL AGENTS, COMPOSITIONS, METHODS AND USES
FILE REFRENCE: CENG945 USA NP
CURRENT APPLICATION NUMBER: US/11/018,102
CURRENT FILING DATE: 2004-12-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.3
SEQ ID NO 25
LENGTH: 110
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APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REPERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR PPLICATION NUMBER: PCT/GB2004/004254
PRIOR PPLICATION NUMBER: GB0324368.0
PRIOR PLING DATE: 2003-10-17
PRIOR PLING DATE: 2003-10-17
NUMBER OF SEC ID NOS: 27
SOFTWARE: Patentin version 3.3
                            PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Pred. No. 7.7e-48;
3; Mismatches 0;
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                                                                                                                                                                   Sequence 10, Application US/10959318; Publication No. US20050215768A1; GENERAL INFORMATION:
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Best Local Similarity 97.3%;
Matches 107; Conservative
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ORGANISM: Artificial
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US-10-959-318-10
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US-11-018-102-25
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LENGTH: 110
  61
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OTHER INFORMATION: Variant of Human 1gG1 CH2 sequence with delta a and d (Q268) OTHER INFORMATION: mutations
                                                                                                                                                                                        APPLICANT: BJUESTONE, JEFFREY A.
APPLICANT: ZIVIN ROBERT A.
APPLICANT: JULUSTONE, JEFFREY A.
APPLICANT: JULUSTONE, JEFFREY A.
APPLICANT: JOLIFFE, LINDA K.
TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
TITLE OF INVENTION: ANTHEROBES
TITLE OF INVENTION: MATHEROBES
TILE REFERENCE: TOLT:0044USC.
CURRENT APPLICATION NUMBER: US/10/267,286A
CURRENT FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
PRIOR PLICATION NUMBER: PCT/US94/06198
PRIOR PLICATION NUMBER: 08/070,116
PRIOR PLICATION NUMBER: 08/070,116
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PALEALIT VET: 2.1
SEQ ID NO 4
LENGTH: 109
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Sequence 7, Application US/10959318

Publication No. US20050215768A1

Publication No. US20050215768A1

Publication No. US20050215768A1

Publication No. US20050215768A1

APPLICANT: Armour, Kathryn L

APPLICANT: Clark, Michael R

TILE REFERENCE: 39-302

TILE REFERENCE: 39-302

CURRENT APPLICATION NUMBER: US/10/959,318

CURRENT PILING DATE: 2004-10-07

PRIOR APPLICATION NUMBER: PCT/GB2004/004254

PRIOR APPLICATION NUMBER: GB0324368.0

PRIOR FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 7

SEQ ID NO 7
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                                                                                                              Sequence 4, Application US/10267286A Publication No. US20030108548A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 97.2'
Matches 106; Conservative
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US-10-959-318-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and d (D268) OTHER INFORMATION: mutations
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Publication No. US2005015/68A1

GENERAL INFORMATION:
APPLICANT: Armour. Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFRENCE: 39-302
CURRENT FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-07
PRIOR PRICATION NUMBER: PCT/GB2004/004254
PRIOR FILING DATE: 2003-10-17
PRIOR PLICATION NUMBER: GB0324368.0
PRIOR PLING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21
LENGTH: 110
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                                                                                APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION Polypeptides including modified constant regions
TITLE OF INVENTION POLYPeptides including modified constant regions
FILE REPERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: PCT/GB2004/004254
PRIOR PILING DATE: 2004-10-07
PRIOR PILING DATE: 2003-10-17
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96.4%; Score 562; DB 18; Length 110;
Best Local Similarity 96.4%; Pred. No. 9e-47;
Matches 106; Conservative 1; Mismatches 3; Indels (
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Pred. No. 9e-47;
3; Mismatches 2; Indels
Sequence 13, Application US/10959318 Publication No. US20050215768A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
SEQ ID NO 13
LENGTH: 110
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Best Local Similarity 95.5%;
Matches 105; Conservative
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ORGANISM: Artificial Sequence
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Gaps

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Indels

Length 110;

Score 559; DB 18; Pred. No. 1.8e-46; 4; Mismatches 2;

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; OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta c and e (E268); OTHER INFORMATION: mutations
US-10-959-318-14
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Best Local Similarity 94.5%;
Matches 104; Conservative
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US-10-959-318-8
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                                                                                                  1 APELLGGPSVFLFPPKPATLMISRTPEVTCVVVDVSQEDPEVKFNWYVDGVEVHNAKTK 60
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| Publication No. US20050215768A1
| Publication No. US20050215768A1
| GENERAL INFORMATION:
| APPLICANT: Armour, Kathryn L. APPLICANT: Clark, Michael R. TITLE OF INVENTION: POLYPEPTIGES including modified constant regions | FILE OF INVENTION: POLYPEPTIGES | CURRENT APPLICATION NUMBER: US/10/959,318
| CURRENT PILING DATE: 2004-10-07 | PRIOR APPLICATION NUMBER: G104-10-07 | PRIOR APPLICATION NUMBER: G203-10-17 | PRIOR PILING DATE: 2003-10-17 | SOFTWARE: Patentin version 3.3 | SEQ ID NO 14 | LENGTH: 110
                                                                           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                0; Gaps
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APPLICANT: Clark, Michael R
TITLE OF INVENTION: POlypeptides including modified constant regions
TITLE REFERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SOUTHARE: Patentin version 3.3
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     Pred. No. 1.4e-46;
3; Mismatches 2; Indels
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Pred. No. 1.5e-46;
2; Mismatches 0; Indels
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  95.58;
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Best Local Similarity 97.3%;
Matches 107; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
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                         Matches 105; Conservative
Best Local Similarity
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US-10-959-318-11
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LENGTH: 109
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OTHER INFORMATION: Variant of Human IgG1 CH2 sequence with delta a and e (E268) OTHER INFORMATION: mutations
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APPLICANT: Clark, Michael R
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR PLICATION NUMBER: PCT/GB2004/004254
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Version 3.3
SEQ ID NO 8
LENGTH: 110
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; Publication No. US20050215768A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Kathryn L
; APPLICANT: Clark, Michael R
; TILE OF INVENTION: POlypeptides including modified constant regions
; FILE REFERENCE: 39-30.
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US/10/959,318
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0324368.0
; PRIOR FILING DATE: 2004-10-07
; PRIOR FILING DATE: 2004-10-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.3
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61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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95.5%; Score 557; DB 18;
Best Local Similarity 94.5%; Pred. No. 2.7e-46;
Matches 104; Conservative 4; Mismatches 2;
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ORGANISM: Artificial Sequence
FEATURE:
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Gaps

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OTHER INFORMATION: Variant of Human 1gG1 CH2 sequence with delta d (Q268) mutation
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PRIOR APPLICATION NUMBER: GB0324368.0 PRIOR FILING DATE: 2003-10-17 SOFTWARE: PATENTIN VERSION 3.3 SEQ ID NO 5 LEID NO 5 LEID NO 5 LEID NO 5 TYPE: PRI
                                                                                                                                                                 ORGANISM: Artificial Sequence
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Matches 102; Conservative
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                                                                                                              OTHER INFORMATION: Variant of Human 1gG1 CH2 sequence with delta a, b and e (E268); OTHER INFORMATION: mutations
US-10-959-318-12
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Publication No. US20050215768A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVENTION: Polypeptides including modified constant regions
FILE REPERENCE: 39-300
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-10-17
PRIOR APPLICATION NUMBER: G80324368.0
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APPLICANT: Armour, Kathryn L
APPLICANT: Clark, Michael R
TITLE OF INVONTION: Polypeptides including modified constant regions
FILE REFERENCE: 39-302
CURRENT APPLICATION NUMBER: US/10/959,318
CURRENT FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: PCT/GB2004/004254
PRIOR FILING DATE: 2004-10-07
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93.9%; Score 547.5; DB 18; Length 109;
Best Local Similarity 94.5%; Pred. No. 2.3e-45;
Matches 104; Conservative 3; Mismatches 2; Indels 1;
                                                                                                                                                                                                          Score 556.5; DB 18; Length
Pred. No. 3e-46;
3; Mismatches 0; Indels
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US-10-959-318-5
Sequence 5, Application US/10959318
Publication No. US20050215768A1
GENERAL INFORMATION:
                                                TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 96.4%;
Matches 106; Conservative
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SOFTWARE: Patentin version 3.3
SEQ ID NO 17
ERNGTH: 109
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ORGANISM: Artificial Sequence
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US-10-959-318-17
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SEQ ID NO 12
LENGTH: 109
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                                                                                             FEATURE:
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